

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OK nucleic - nucleic search, using sw model

Run on: April 15, 2003, 00:16:08 ; Search time 4340.53 Seconds

(without alignments)
10987.631 Million cell updates/sec

Title: US-09-001-737-7_COPY_15_1652

Perfect score: 1638

Sequence: 1 ATGCCAAGAGATCAATTT.....TGGGTGGATGCGCGATRA 1638

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database: GenBank

Listing first 45 summaries

```

1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_in:*
18: em_mu:*
19: em_om:*
20: em_or:*
21: em_ov:*
22: em_ph:*
23: em_pat:*
24: em_pl:*
25: em_pi:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlg_mus:*
34: em_hlg_pia:*
35: em_hlg_rdg:*
36: em_hlg_mam:*
37: em_hlg_vtl:*
38: em_sy:*
39: em_hlg_hum:*
40: em_hlg_mus:*
41: em_hlg_other:*

```

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1620.2	98.9	10389	1	AE006627
2	1605.8	98.0	53291	1	AE014170
3	1602.6	97.8	11576	1	AE010115
4	1413.4	86.3	2683	6	SPGROELGN
5	1413.4	86.3	2683	6	AX148805
6	1102.8	71.5	1421	1	AX121365
7	1100.4	69.6	1306	6	AX148806
8	1128.8	68.9	1421	1	AX121364
9	1125	68.7	1422	1	AX121366
10	1122.6	68.5	1395	6	AX148809
11	1118	68.3	1425	1	AX121367
12	1104.2	67.4	2024	1	AX121368
13	1075.4	65.7	2324	1	AX121369
14	1073.4	65.7	2324	1	AX121370
15	1068.2	65.2	2320	1	AX121371
16	1063.6	64.9	2020	1	AX121372
17	1052.8	64.3	1718	1	AX121373
18	1050.4	64.1	2639	1	AX121374
19	1039.2	63.4	1623	6	AX121375
20	1038.4	63.4	1623	6	AX121376
21	1038.4	63.4	1623	6	AX121377
22	1037.6	63.3	21494	2	SPNEU1924
23	1036	63.2	1647	6	AX121378
24	1036	63.2	2107	6	AX121379
25	1036	63.2	2107	6	AX121380
26	1034.4	63.2	5365	6	BD003757
27	1034.4	63.2	11318	1	AE008538
28	1034.4	63.2	13103	1	AE007482
29	1029.6	62.9	2401	6	AX148801
30	1029.6	62.9	2401	6	AX148802
31	1013.6	61.8	2401	6	AX148803
32	1012.4	61.8	2401	6	AX148804
33	1012.2	61.8	1963	1	AE008276
34	954.2	58.3	12560	1	AE008277
35	947.8	57.9	2267	1	AE008278
36	942	57.5	3120	1	AE008279
37	941.4	57.5	2187	1	AE008280
38	844.6	51.6	2853	1	AB073399
39	839.4	51.2	2834	1	AB073400
40	837.8	51.1	2309	1	BACSGROEST
41	831.2	50.7	1901	6	AX148805
42	823.2	50.3	213251	6	AX148806
43	823.2	50.3	213251	6	AX148807
44	821.6	50.2	2156	1	AF335323
45	821.6	50.2	295050	1	AL591982

ALIGNMENTS

RESULT 1
LOCUS AE006627 10389 bp DNA linear BCT 01-JUN-2001
DEFINITION Streptococcus pyogenes M1 GAS strain SF370, section 156 of 167 of
the complete genome.
ACCESSION AE006627 AE004092
VERSION AE006627.1 GI:13623059
KEYWORDS
SOURCE Streptococcus pyogenes M1 GAS.
ORGANISM Streptococcus pyogenes M1 GAS.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
REFERENCE
1 (bases 1 to 10389)
Ferretti J.J., McShan W.M., Adl J.C., Savic G., Lyon K.,
Primeaux C., Seaton S.S., Surov A.N., Kenton S., Lal H., Lin S.,

FEATURES	SOURCE
TITLE	Qian, Y., Jia, H.G., Najaf, F.Z., Ren, Q., Zhu, H., Song, L., White, J., Yuan, X., Clifton, S.W., Roe, B.A. and McLaughlin, R.E.: Complete genome sequence of an M1 strain of <i>Streptococcus pyogenes</i> Proc. Natl. Acad. Sci. U.S.A. 98 (8), 4658-4663 (2001)
JOURNAL	11293684
MEDLINE	11293684
PUBMED	112936296
REFERENCE	2 (bases 1 to 10389)
AUTHORS	Ferrecci, J.J., Moshan, H.M., Adji, C.D., Savic, D., Savic, G., Lyon, K., Plameaux, C., Sezter, S.S., Suroroy, A.N., Kenton, S., Lai, H., Lin, S., Qian, Y., Jia, H.G., Najaf, F.Z., Ren, Q., Zhu, H., Song, L., White, J., Yuan, X., Clifton, S.W., Roe, B.A. and McLaughlin, R.E.
TITLE	Direct Submission
JOURNAL	Submitted (10-Apr-2001)
FEATURES	Department of Microbiology and Immunology, University of Oklahoma Health Sciences Center, 940 St Young Blvd, Oklahoma City, OK 73104, USA
SOURCE	Location/Qualifiers I. .10389

gene
CDS
/organism="Streptococcus pyogenes M1 GAS"
/strain="SP370"
/serotype="M1"
/db_xref="taxon:160490"
complement(75..1799)
/gene="Spy2065"
complement(175..1799)
/gene="Spy2065"
/note="Best Blastp hit = pf112109195a chondroctin ABC
lyase [proteus vulgaris]"
/codon_start=1
/transl_table=1
/product="Hypothetical protein"
/protein_id="AAK34725.1"
/db_xref="GI:13623060"
/translation="MMYLGFENPEAIAYDIYKKNIESMGLMTPEKHHKTLKOTITIT
AATSLILGICGAFYSGKNCINAVLAIAOAGSPFENICAYVMDTNDITDPE
MYTRRRRSYDLEKROKODLKAASOSAVOYKSGRRMFPDRIATKPMDLTKT
VQAVLNLONKQKVAVDSQSPVLDRPLAEYTAISGKNGNINIKYSDLTG
LDLSVPTFTEFLVSNKOGDLEPDNHLIGTLKQLOVEDPVTENAKMTKTPD
ELSRQVALDVEGATLELLIYVTLLEPKAGELVAFDQMHITLSTGDSNNRS
FAGSNNAPFRLGKSEIKRQTPTRKASNLHLSLITLITGVKTYVLDFTATPE
FLYDSTDPHOPSGHINDLTGVTYKKGQHTLISQSGKNLTAVKEDNLTAV
PESTICISGQANGSLHMSLSDGTTIKVEDKGRNSERTAKISKVDKNGNS
VLYTPDQSDLSLAVPEGGLGAVNKAYGFIKISRTASPVMAQLTHEFTPTPLS
GTYLQKQ"
1962..3458
/gene="Spy2066"
1962..3458
/gene="Spy2066"
/note="Best Blastp hit = emb|CAA66893.1| (X98238)
putative; orf1 [lactobacillus sakei]"
/codon_start=1
/transl_table=1
/product="putative dipeptidase"
/protein_id="AAK34726.1"
/db_xref="GI:13623061"
/translation="MINKISLVSLTAFSLQSVACNGFIIIGKDLTKDGSILYG
KTELEAHNKNIVLRANKDPAEKMKDLSNGEYPLPEHSYSAIPDVPKRGVY
DEAFTEGGAEGSVASVANDAIQKIDPYVNGIAESMTSVILPSVTAAREGALIT
IKAYEENAGSIVATLADKGIYWEILLSGQYVAIFPDQDYAVFPPTFGLHDF
NDKNTKASNEVLLDSTKDFSLQDMARKLQNRNEGGLDPLDQALDQSGFKSRKAY
KYAPISNPVWEAHIPOLKCDIPAEIGCVMLSGSRRNAPFLPIDGINSITVEAO
GYATVQDKNKGWVSHINDLVAAHPRPGVTIDENKKGELTWIENEDKSKRISDL
VLSPPKAQKQKDKISLRAKTEPKRLKAIETAKVTEKPKNGKGLNRS"
complement(4661..6592)
/gene="groEL"
/note="Spy2070"
complement(4661..6592)
/gene="groEL"
/note="The N-terminal amino acid sequence of this ORF has
been determined from a spot isolated by 2-D gel
electrophoresis from another strain of S. pyogenes. Hogan,
D. A., Whittton, M. M., Rogers, J. and R. A. Vangogelen.
2000. Two-dimensional gel electrophoresis map of

Streptococcus pyogenes proteins. Unpublished data.: Best Blastp hit = emb|CAA61530.11 (X89236) heat shock protein [Streptococcus pyogenes]"

/codon_start=1
/transl_table=1
/product="heat shock protein (chaperonin)"
/protein_id="AAK34727.1"
/db_xref="GI:13633062"
/translation="MAKQKRSADARAARVGVDMADLYKVTGLGKGRNVLEKAFG
SPILNDPVTATETEDMEENMGAKLVSEVASTNDLIGDSTTATVLTQALVHG
LKNAVQVNPGRIGETRTKINAVELKAKIOPVSGEKIALQAVASRSEKGEYI
SPAMRVGNQGVTESEHSGMETELEVSESGMDGTISQVPTWDEKMWADLENPI
LITDCKRPNVODIPLLESEVLTNRPLLIITADVDVGLPVLVTLNKIGTNNVAVKA
GSEBPLANRILRLSOLLETTGVTEDEGKLEDAVNRALQAAKTVKDSYTVGSA
RIEDLAAVNRILRSLQVTEVAGGATLITVLEAKALEGSDAAGRITVALRLEPPO
ILNANGISGVYIDKLNSPAGTGSFNAAGVEWVDITGIDIPDKVTRSLALQNAVA
SLITLEVAAKPEEPAARMAPAGMDQPMWGG"

complement(6528. , 6618)
/gene="groES"
/note="SpY2072"
complement(6328. , 6618)
/gene="groES"
/note="The N-terminal amino acid sequence of this ORF has
been determined from a spot isolated by 2-D gel
electrophoresis from another strain of *S. pyogenes*. Hogen,
D. A., Whittion, M. M., Rogers, J. and R. A. Vanobeglen,
2000. Two-dimensional gel electrophoresis map of
Streptococcus pyogenes proteins. Unpublished data.; Best
Blastp hit = gb|AAF75592.1|AF214488_2 (AF214488) GroES
[Lactobacillus johnsonii]"
/codon_start=1
/transl_table=1
/product="heat shock protein - cochaperonin"
/protein_id="AAK34728.1"
/db_xref="GI:13623063"
/translation="MLKRIQDPRVVRFPDEKQVGGFVLACTHRESKRAITYLASE
TGVRTIGDSVTPSYSGQPELVENHDLFTVDDENVSTINESDIIATVTK"
complement(6796. , 9240)
/gene="clpC"
/note="SpY2073"
complement(6796. , 9240)
/gene="clpC"
/note="Best Blastp hit = gb|AAC44446.11 (U40604) ClpC
ATPase [Listeria monocytogenes]"
/codon_start=1
/transl_table=1
/product="putative endopeptidase Clp ATP-binding chain C"
/protein_id="AAK34729.1"
/db_xref="GI:13623064"
/translation="MIMVSTKMODIFRQAFQFQARFDSHCLETWHVLLAVAVDMSLA
NMILSEVDQAVVIEVEEAAAILAMGCTRPEDLSVDFPROSGSTLTNLNFAQASITL
RDQGVSEHLEVALIILNPDIIMASRLLEIAGVQIKDNGNQPDLADLKAIEBHAQYK
EMIAEHLERKRTKQGTGFPDMKPPSTGELSGPTNDLLEAAROGCILEYIGRD
EVSIMLOVSRTEENNNQIIDIDLEADGQIILFYDELHTLTMSSGSDISTDLAANTLR
SVAGTGFSPKDEENNNQIIDIDLEADGQIILFYDELHTLTMSSGSDISTDLAANTLR
ALSHGTHAVGTOETEOKRIEKLDAISREKATLIEPNEENQAYIIMGLAKLEYR
YHANGISNAVTAVMKHAHLEKSLNLDPSALDOLBASAANQWMAVYKLEFELV
OALINDMKVIGSDAALAEAKGCMRRPPEVDDIITLTKSGIPKRLQDMSKIL
NLEKEHLKVVISDLEMEVEWKEPASAIRNCPGCVGTDSDEGLQVNGKTELMKAL
AEVLPFDEALIRIDMEVEWKEPASAIRNCPGCVGTDSDEGLQVNGKTELMKAL
DEVKRAHDPFVILVOLDGCTILTSRCKAYDSNLIITNSIATGALMDKVTGVS
VKQIHODHQAOKRLHELEKTYRPEFYNRIDEVVFNHSLQDMNRVAKIVQVLT
TLAEKTIITLQAPLAKHLESGVDEHMGAPLRLKLTQLEIDKLSELLISRELTSGH
TKLIGSHKRLTETHA

complement(9240. , 9701)
/gene="csr"
/note="SpY2074"
complement(9240. , 9701)
/gene="csr"
/note="Best Blastp hit = sp|P37568|CTSR_BACSU
TRANSCRIPTIONAL REULATOR CTSR >g|2127052|p|ir|566112
transcription repressor csr - Bacillus subtilis

```

>g1467471|dbj|BA05317.1| (D26185) unknown [Bacillus
subtilis] >g112632350|emb|CAB11859.1| (299104)
transcriptional regulator [Bacillus subtilis]
/codon_start=1
/transl_table=11
/product=putative transcriptional regulator
/protein_id=AK34730.1
/db_xref=GI:13623065
/translation=HPTKNTSDSIEBYIKELLSIAEIKRSMIADSEQVYPSOIN
YIKRTESRGTEVESKRGGGGIRIAKVFSDKHHILGNLMATIEDCISEQVFTDSI
QLEPDELTEREGNIIILAVASDVLGTDSITRIAMLYRLRORIDRKSNN
complement(9897, 10100)
/gene=csp
/feature=SPY2077
complement(9897, 10100)
/gene=csp
/feature=Best Blastp hit = emb|CA76697.1| (Y17216) cold
shock protein D [Lactococcus lactis]
/codon_start=1
/translation=1
/product=putative cold shock protein
/protein_id=AK34731.1
/db_xref=GI:13623066
/translation=MAQSTYKMFNENKGFISTENGQDVAFHSAIOTNGKILEEG
OKVAFPEVGEGRQHPQAVNITKLA
BASE COUNT 3077 a 2210 c 1855 g 3247 t
ORIGIN

Query Match 98.9%; Score 1620.2; DB 1; Length 10389;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1622; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGCAAAAGAAATCAAAATTTTCAGCAGATGCGCGTGTGCGAGCGGATGAT 60
DB 6292 ATGGCAAAAGAAATTTAAATTTTCACAGATGCGCGTGTGCGAGCGGATGAT 6233
QY 61 ATGTAGCAGATACCGTCAAAAGTAAACGTTGCTCTAAAGGCGCAATTTGCTTGA 120
DB 6332 ATGTAGCAGATACCGTCAAAAGTAAACGTTGCTCTAAAGGCGCAATTTGCTTGA 6173
QY 121 AAAGCTTTGGTCTCCTTAATTAATGAAGGAGGATTAACCATTTCTAAGAGATGAA 180
DB 6172 AAAGCTTTGGTCTCCTTAATTAATGAAGGAGGATTAACCATTTCTAAGAGATGAA 6113
QY 181 TTGAAGATCAATTTTGAACATGAGGAGGATTAACCATTTCTAAGAGATGAA 240
DB 6112 TTGAAGATCAATTTTGAACATGAGGAGGATTAACCATTTCTAAGAGATGAA 6053
QY 241 AATGATATTGCTGTATGAGGAGGATTAACCATTTCTAAGAGATGAA 300
DB 6052 AATGATATTGCTGTATGAGGAGGATTAACCATTTCTAAGAGATGAA 5993
QY 301 GAAGGACTAAAAATGTGACAGCGTCTAATCCATTTGATCCGTGAGGATGAA 360
DB 5992 GAAGGACTAAAAATGTGACAGCGTCTAATCCATTTGATCCGTGAGGATGAA 5933
QY 361 ACAGCAACAGCAACAGCTTGAAGCCTTGAAGCCTTGAAGCCTTGAAGCCTTGAAG 420
DB 5932 ACAGCAACAGCAACAGCTTGAAGCCTTGAAGCCTTGAAGCCTTGAAGCCTTGAAG 5873
QY 421 GAAGCTATTGCTGAGCTGCTGAGTATCATCAGCTCTGAAAGAGTGAAGTATATC 480
DB 5872 GAAGCTATTGCTGAGCTGCTGAGTATCATCAGCTCTGAAAGAGTGAAGTATATC 5813
QY 481 TCAGAAAGTATGAGGCTGTGGGCAAGATGATGATACCATGAGATTCAGAGT 540
DB 5812 TCAGAAAGTATGAGGCTGTGGGCAAGATGATGATACCATGAGATTCAGAGT 5753
QY 541 ATGGAACAGAACTGAAGTGTGAAGGATGCAATTTGACCGTGTGTACCTGTCTCA 600
DB 5752 ATGGAACAGAACTGAAGTGTGAAGGATGCAATTTGACCGTGTGTACCTGTCTCA 5693
QY 601 TACATGCTCAGACAAATGAAAAATGTTGCAAGCTTGAAGCCATTTATCTTAATC 660

```

```

DB 5692 TACATGCTCAGACAAATGAAAAATGTTGCAAGCTTGAAGCCATTTATCTTAATC 5633
QY 661 ACGATATAAAAGTGTCAACATCAAGACATTTTGGCACTACTTGTAGAGATCTTA 720
DB 5632 ACGATATAAAAGTGTCAACATCAAGACATTTTGGCACTACTTGTAGAGATCTTA 5573
QY 721 ACCAAGCTCATTAATCATTAATGATGATGATGATGATGATGATGATGATGATGAT 780
DB 5572 ACCAAGCTCATTAATCATTAATGATGATGATGATGATGATGATGATGATGATGAT 5513
QY 781 GCTTGAACAAGATTCGTGACTTCAATGATGATGATGATGATGATGATGATGATGAT 840
DB 5512 GCTTGAACAAGATTCGTGACTTCAATGATGATGATGATGATGATGATGATGATGAT 5453
QY 841 GATGCTGAAGATTCGTGACTTCAATGATGATGATGATGATGATGATGATGATGAT 900
DB 5452 GATGCTGAAGATTCGTGACTTCAATGATGATGATGATGATGATGATGATGATGAT 5393
QY 901 GAGATTCAGACCTTGAATTAAGATGCTAATGACAGCCCTTGGACAGCTGTAG 960
DB 5392 GAGATTCAGACCTTGAATTAAGATGCTAATGACAGCCCTTGGACAGCTGTAG 5333
QY 961 ATTACAGTATTAAGATGACAGTAAATTTGTAAGTTCAGAGAGTTCAGAGCTAT 1020
DB 5332 ATTACAGTATTAAGATGACAGTAAATTTGTAAGTTCAGAGAGTTCAGAGCTAT 5273
QY 1021 GCTAACCTATTGCACTGATTAATGCAATTAAGAAACAACACTTGCATTTGACGT 1080
DB 5272 GCTAACCTATTGCACTGATTAATGCAATTAAGAAACAACACTTGCATTTGACGT 5213
QY 1081 GAAAACTACAGAGCTTTGGGAAATTAAGTGTGATGATGATGATGATGATGATGAT 1140
DB 5212 GAAAACTACAGAGCTTTGGGAAATTAAGTGTGATGATGATGATGATGATGATGAT 5153
QY 1141 GCTCAAGAGACAGCTTTAAAGAAATGCAATTCGATGAGATGCTCTAAATGCT 1200
DB 5152 GCTCAAGAGACAGCTTTAAAGAAATGCAATTCGATGAGATGCTCTAAATGCT 5093
QY 1201 ACAGTGCAGCCGTTGAAGAGTATCGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
DB 5092 ACAGTGCAGCCGTTGAAGAGTATCGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 5033
QY 1261 ATTGAAGATGACAGCTCTTGAAGCTTGAAGGCGATGATGCTATGACATTAATG 1320
DB 5032 ATTGAAGATGACAGCTCTTGAAGCTTGAAGGCGATGATGCTATGACATTAATG 4973
QY 1321 CTTGCTGCTCTGAAGAGCCTGTAGCTCAATTTGTAATGCTGCTGCTGCTGCTG 1380
DB 4972 CTTGCTGCTCTGAAGAGCCTGTAGCTCAATTTGTAATGCTGCTGCTGCTGCTG 4913
QY 1381 GTAGTATTGACAGTGAAGAAACAGCCCTGACAGAAAGATTAATGCTGACAGCT 1440
DB 4912 GTAGTATTGACAGTGAAGAAACAGCCCTGACAGAAAGATTAATGCTGACAGCT 4853
QY 1441 GATGAGTGTGATGATTAACAGAGATCATTTGACCTGCAAGAAAGTAAACAGATCAG 1500
DB 4852 GATGAGTGTGATGATTAACAGAGATCATTTGACCTGCAAGAAAGTAAACAGATCAG 4793
QY 1501 CTTCAAAATGACGCTTCTGAGTATTTTATTTTACACAGAGAGTGTGCTAAT 1560
DB 4792 CTTCAAAATGACGCTTCTGAGTATTTTATTTTACACAGAGAGTGTGCTAAT 4733
QY 1561 AAACCTGAACAGCTACGCGACGACAGCAATCCACAGAGATGATGATCAGAGATG 1620
DB 4732 AAACCTGAACAGCTACGCGACGACAGCAATCCACAGAGATGATGATCAGAGATG 4673
QY 1621 GGTGG 1625
DB 4672 GGTGG 4668

```

RESULT 2

	AE014170/C	53291 bp	DNA	linear	BCT 19-JUL-2002
LOCUS	Streptococcus pyogenes MGAS315, section 35 of the complete genome				
DEFINITION	AE014170 AE014074				
ACCESSION	AE014170.1 GI:21905475				
VERSION					
KEYWORDS	Streptococcus pyogenes MGAS315.				
SOURCE	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;				
ORGANISM	Streptococcus				
REFERENCE	1 (bases 1 to 53291)				
AUTHORS	Beres,S.B., Sylva,G.L., Barblan,K.D., Lei,B., Hoff,J.S., Kammrille,N.D., Liu,M.-Y., Smoot,J.C., Porcella,S.F., Parkins,L.D., McCormick,J.K., Leung,D.Y.M., Schlievert,P.M. and Musser,J.M.				
TITLE	Genome sequence of a serotype M3 strain of group A Streptococcus: Phage-encoded toxins, the high-virulence phenotype, and clone emergence				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (15), 10078-10083 (2002)				
REFERENCE	2 (bases 1 to 53291)				
AUTHORS	Beres,S.B., Sylva,G.L., Barblan,K.D., Lei,B., Hoff,J.S., Kammrille,N.D., Liu,M.-Y., Smoot,J.C., Porcella,S.F., Parkins,L.D., McCormick,J.K., Leung,D.Y.M., Schlievert,P.M. and Musser,J.M.				
TITLE	Direct Submission				
JOURNAL	Submitted (14-JUN-2002) Laboratory of Human-Bacterial pathogenesis, Rocky Mountain Laboratories, NIAID, NIH, 903 South Fourth St., Hamilton, MT 59840, USA				
FEATURES	Location/Qualifiers				
source	1..53291 /organism="Streptococcus pyogenes MGAS315" /strain="MGAS315" /serotype="M3" /db_xref="taxon:198466" /note="group: A" complement(162..3671) /gene="scpa" /note="Spym3_1726" complement(162..3671) /gene="sepa" /note="best blastcp hit: sp P15926 SCA1_STRPY_CSA peptidase precursor (SCP)" /codon_start=1 /transl_table=1 /product="CSA peptidase precursor" /protein_id="AAH80333.1" /db_xref="GI:21905476"				
gene	/translation="MRKQKLPEFKLALALMSTSLILMAOSDIKANVTEDTPATEOA VEPPOQTASEAPSSSSSEKPNPTDDAEFVADKANDLAQAPATAATPATPSKE TIDLNDSDSHVKTLQEKAGSGAVIVADIGDNHEARLDKRSKRSEDEK AKKDHDITGEMVDNKAYIHHDSKGTAVOEHGTGVLISGNAPSREPLE GAPEKKLLMRVINYGLADYANRYAOAIRBVALGAKNINSNGMALAYLVNLYS TKAFPAYSKGVSIYTSAGNSDSEFGKRLDLADHDVGTVTSPRAADSTRIVADE PDQLPERATKTADDOCKEMPVISTNRREPKEADVAVANRQCTEDENPRKTKAL IESGDLEDKRIANAKKAAGVILIYNDRPKPELPELVANRQCPAATSRDGLIKL NSKTTTNTPAPVLPPLTASCTLSRSPSKSLADNTIKIPDAIRCDLITSYANKKYA KLSGSMSAPLVAGINGILLQKOYETROPMTSEPELDAKUUMASAALIDEKAY FSPROOGAGVADKAKAATVYNDKNTSSVHLNNYSOKPEVITYAHNSKRPDEL YTOATPDODKDGHPALAPALKTEPMOKITFPANSKQVITYIDASKRKOLLM KNVELEPFERKDPDTRELMSPIPIGRHDFGMLSLKRPYDSKGSYTHENS DAIKDOLDGGIETALAKNFTHLTIESNPITTIKAVEENLEDIESSETLETAG TRAKDODSHHTIRHANGRPALAISPDNGRDYVPGQETPLANNALVAELVDGE DYVNIIEVYBNVNNNDLASTJASTREKTRMDGDKDGVANGVYTYRVRYTPY ISSAKQRHDDVAVNDTPENASTASFSEHEDRRUTLASPKTSGVYRERIATYMD EDLPTEETISENEDGITPELPEATBMKGATVLSKSDPTVVVEDAGNVITYETNL EGSNNPFDGSDSDVDKTFPEKPEDGSGQAPDKPEANPECDSDGAPDKPETRK EKXSSSQDGTQKQGPSRTLEKRSSKRALATKASARDLPTINDKTDNLHLKLV MTFEFGVAHIETKROKETK"				
CDS	complement(401..5786) /gene="emm3" /note="Spym3_1727"				
gene	complement(401..5786) /gene="emm3" /note="Spym3_1727"				
CDS	complement(4041..5786)				

D	44705	TTGAAGATCAATTTTAAAAACATGGGACGCAAAATTTGGTGTCTGAAGTGGCTCTTAAACC	44646
O	241	AATGATATTCGTGTATGGAGACACTACTGTGAACATTTTATGACACAGCAATTTGCAT	300
D	44645	AATGATATTCGTGTATGGAGACACTACTGTGAACATTTTATGACACAGCAATTTGCAT	44586
O	301	GAGGACTTAAAAAATGTGACAGAGGTGTATGCATTTTGTATCCGTGAGGCAATGAA	360
D	44585	GAGGACTTAAAAAATGTGACAGAGGTGTATGCATTTTGTATCCGTGAGGCAATTTGA	44528
O	361	ACGCAACAGCAACACTGTTGAAGCCTGGAACCCATTTGTCACACTGTATCTGGCAG	420
D	44525	ACGCAACAGCAACACTGTTGAAGCCTGGAAGCCTGGAAGCCATTTGTCACACTGTATCTGGCAG	44466
O	421	GAGGCTATTCGTGTATGGTGTGCTGCGACGATATCAACGCTCTGAAAAGTTGGAGATATTC	480
D	44465	GAGGCTATTCGTGTATGGTGTGCTGCGACGATATCAACGCTCTGAAAAGTTGGAGATATTC	44406
O	481	TCGAGCGTATGAGAGCTGTGTGGCAACCATGTTGATTTACCTGCAAGATCTCGAGT	540
D	44405	TCGAGCGTATGAGAGCTGTGTGGCAACCATGTTGATTTACCTGCAAGATCTCGAGT	44346
O	541	ATGGAACAGACTTGAAGTGTGGAAGCAATTTGACCGTGTATTCCTGTCTCA	600
D	44345	ATGGAACAGACTTGAAGTGTGGAAGCAATTTGACCGTGTATTCCTGTCTCA	44286
O	601	TGATGTGTACAGACATGAAAAAATGTTTGCAGACCTTGAAGAACCCATTATCTATC	660
D	44285	TGATGTGTGTACAGACATGAAAAAATGTTTGCAGACCTTGAAGAACCCATTATCTATC	44226
O	661	ACGGAATAAAAGTGTCAACATCCAGCATTTTCCCACTACTTGGAGAAATTCCTTAA	720
D	44225	ACGGAATAAAAGTGTCAACATCCAGCATTTTCCCACTACTTGGAGAAATTCCTTAA	44166
O	721	ACCAACGTCATTACTACTATTAATGTGAGATGATGTGAGGAGAGCACTGTCCAAACCCT	780
D	44165	ACCAACGTCATTACTACTATTAATGTGAGATGATGTGAGGAGAGCACTGTCCAAACCCT	44106
O	781	GCTCTGAACAAGTTCGCGGACTTTTCAATGTGGTGTGCTGCAAGGCGCAGATTTGGT	840
D	44105	GCTCTGAACAAGTTCGCGGACTTTTCAATGTGGTGTGCTGCAAGGCGCAGATTTGGT	44046
O	841	GATCGGTGAAGCTATGCTTGAAGCATGTCATGATGAGAGGTGTACAGTATTAAC	900
D	44045	GATCGGTGAAGCTATGCTTGAAGCATGTCATGATGAGAGGTGTACAGTATTAAC	43986
O	901	GAGGATCAGGACTGTAATTAAGTGTCTCAATGACGCCCTTGGACAGGCTGTAG	960
D	43985	GAGGATCAGGACTGTAATTAAGTGTCTCAATGACGCCCTTGGACAGGCTGTAG	43926
O	961	ATTAACATGTATTAAGATACGACAGTAATTTGTTGAAGTTCGAGAAATTCAGAAAGTATT	1020
D	43925	ATTAACATGTATTAAGATACGACAGTAATTTGTTGAAGTTCGAGAAATTCAGAAAGTATT	43866
O	1021	GCTAACCGTATTCGACTGATTAATTCGACATTTAGAAACACACATTTCTGACTTTGACCGT	1080
D	43865	GCTAACCGTATTCGACTGATTAATTCGACATTTAGAAACACACATTTCTGACTTTGACCGT	43806
O	1081	GAAAAACTACAAAGACGTTTGGCGAAATATAGCTGTGTGACTGTTTACAAAGTAGA	1140
D	43805	GAAAAACTACAAAGACGTTTGGCGAAATATAGCTGTGTGACTGTTTACAAAGTAGA	43746
O	1141	GCTCAACAGACAGTGTAAAAAATAAATAAATCTGCATGTAGAGATGCTTAAATGCT	1200
D	43745	GCTCAACAGACAGTGTAAAAAATAAATAAATCTGCATGTAGAGATGCTTAAATGCT	43686
O	1201	ACAGGTGACGCGTTGAAGAGCTTCTGCTGTGCTGTGTGGAACACACTTATACGTT	1260
D	43685	ACAGGTGACGCGTTGAAGAGCTTCTGCTGTGCTGTGTGGAACACACTTATACGTT	43626
O	1261	ATTGAAAAAGTAGCAGCTTGTAGCTTGAAGGCGATGATGCTTACGTGACGTAACTATTGTG	1320

Db 43625 ATGAAAAGTAGACGCTCTTGAACTTGAGGCGCATGATGCTACTGAGCTAACTATGTG 43566
Oy 1321 CTTGCTGCTAGTAGAGAGCCCTGTACGTCAAAATGCTTAAATGCTGGTAGCAAGCTCC 1380
Db 43565 CTTGCTGCTAGTAGAGAGCCCTGTACGTCAAAATGCTTAAATGCTGGTAGCAAGCTCC 43566
Oy 1381 GTAGTTATTTGACAGTTGAAAAACAGCCCTGCGAGACAGATTAAATGCTCAACAGCT 1440
Db 43505 GTAGTTATTTGACAGTTGAAAAACAGCCCTGCGAGACAGATTAAATGCTCAACAGCT 43446
Oy 1441 GAGTGGTTGATGATGATTAAGAGAAATGATGAGCCTGCTCAAAATGATGATGATG 1500
Db 43445 GAGTGGTTGATGATGATTAAGAGAAATGATGAGCCTGCTCAAAATGATGATGATG 43386
Oy 1501 CTTCAAAATGACAGCTTCTGTAGCTTATGCTTATTTGACACAGACAGCACTGCTTAT 1560
Db 43385 CTTCAAAATGACAGCTTCTGTAGCTTATGCTTATTTGACACAGACAGCACTGCTTAT 43326
Oy 1561 AACTGTAACACAGCTTCTGTAGCTTATGCTTATTTGACACAGACAGCACTGCTTAT 1620
Db 43325 AACTGTAACACAGCTTCTGTAGCTTATGCTTATTTGACACAGACAGCACTGCTTAT 43266
Oy 1621 GGTGG 1625
Db 43265 GGTGG 43261

RESULT 3
AE010115/c 11576 bp DNA linear BCT 03-APR-2002
LOCUS Streptococcus pyogenes strain MGAS8232, section 163 of the
DEFINITION complete genome
ACCESSION AE010115 AE009949
VERSION AE010115.1 GI:19749196
KEYWORDS
SOURCE Streptococcus pyogenes MGAS8232.
ORGANISM Streptococcus pyogenes MGAS8232.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
REFERENCE 1 (bases 1 to 11576)
AUTHORS Smoot,J.C., Barbican,K.D., Van Gompel,J.J., Smoot,L.M.,
Chaussee,M.S., Sylva,G.L., Sturdevant,D.E., Ricklefs,S.M.,
Porcella,S.F., Parkins,L.D., Beres,S.B., Campbell,D.S., Smith,T.M.,
Zhang,Q., Kapur,V., Daly,J.A., Veasy,L.G. and Musser,J.M.
TITLE Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
outbreaks
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (7), 4668-4673 (2002)
MEDLINE 21927593
PUBMED 11917108
REFERENCE 2 (bases 1 to 11576)
AUTHORS Smoot,J.C., Barbican,K.D., Van Gompel,J.J., Smoot,L.M.,
Chaussee,M.S., Sylva,G.L., Sturdevant,D.E., Ricklefs,S.M.,
Porcella,S.F., Parkins,L.D., Beres,S.B., Campbell,D.S., Smith,T.M.,
Zhang,Q., Kapur,V., Daly,J.A., Veasy,L.G. and Musser,J.M.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-2002) Laboratory of Human Bacterial
Pathogenesis/Rocky Mountain Laboratories/NIH/NIH, 903 S. 4th St.,
Hamilton, MT 59840, USA
FEATURES
Source
1. 11576
Location/Qualifiers
/organism="Streptococcus pyogenes MGAS8232"
/strain="MGAS8232"
/db_xref="taxon:186103"
misc_feature
/note="spvM18_2128: probable gene fragment; best blastp
match db|BA05200.1| (AB025228) rrg [Streptococcus
orailis]"
gene
complement(535..2166)
/gene="groL"
/note="spvM18_2129"
complement(535..2166)
/gene="groL"
CDS
/gene="groL"

gene
complement(365..6109)
/gene="clp"
/note="spvM18_2134"
complement(365..6109)
/gene="clp"
/note="best blastp match gb|AAK34729.1| (AE006627)
putative endopeptidase Clp ATP-binding chain C
[Streptococcus pyogenes M1 GAS]"
/codon_start=1
/transl_table=11
/product="putative endopeptidase Clp ATP-binding chain C"
/protein_id="AAJ98584.1"
/db_xref="GI:19749200"
/translation="MIMSTKMDIFRQAFQARFDSHLETHVLLANVAVDSLA
NMLSEIDAOVALEETEAAALILNPDIMASLLEIGQOINONQOPRLADRLAEIAGYSK
EKIKAIHELKRPKPKTKGTGSDMKPSTAGSELDFDRLDMAROGLEISVIGDQ
EVSRRIVOLSRKTKNNPVLVDAGVKTALVGAQIANGAIPVLEKERNVLEIDM
SVNACTFRGDFEERNQIIDDIEADGQIILFVDELITNGSGSISDTDAANILKPK
ALASRGLHWGATQIEYQKIEKDALSRRAKILIEPNTEDAYOILGKLKLYET
YNNVISNEAVKTAVKNAHRYLTKMLPDSALIDLDASAAYAVONNVKSSAPETIPI
DALNGMKVSRLLAKKAGKORRPTPTEDDILATLSEKLGIPLEKLRADSKYL
NLELHKRVIGQDAAVTAISRAIRRNQSGIRTKRPISSPFIAGPTGVKELKAL

gene
complement(2202..2492)
/gene="groS"
/note="spvM18_2131"
complement(2202..2492)
/gene="groS"
/note="best blastp match gb|AAK34728.1| (AE006627) heat
shock protein - co-chaperonin [Streptococcus pyogenes M1
GAS]"
/codon_start=1
/transl_table=11
/product="heat shock protein - co-chaperonin"
/protein_id="AAJ98582.1"
/db_xref="GI:19749198"
/translation="MLKPLGDRVVRVRFDEKEQVGVLAGTRKSRKATVAVSE
TGVRITDSDVLPESVSGEVLVENGHLEVTVDDEKYSIIRSDIATVK"
2740..3582
/gene="tra"
/note="spvM18_2133"
2740..3582
/gene="tra"
/note="best blastp match gb|AAJ59388.1| (U11799) putative
transposase [Streptococcus pyogenes]"
/codon_start=1
/transl_table=11
/product="putative transposase"
/protein_id="AAJ98583.1"
/db_xref="GI:19749199"
/translation="MGDIYTPKQQLTIHERROIQRLKLSRNEIARLIGRAPOTI
HNEIKRGLVROVRKKEFEAVYSAGHOLVYQENKRSPPRIKORQOREAIEHYRO
NYSPEIVKAKGVQVPSVITYWHQKLSLCKEMLYPRKAKARAKASPRKAPAGK
NIEORPDSINORLEAGHVEIDTVILTPAKNOCLLTLDRTKTHQILRIIPKSAQAVN
KALGILKDYVNSITADNGTEFSLSDVSLKVPKRPKLKSLILNIGSITILNDSST
TSRO"

```

AEVLDEDEALIRFDMSEYMERFAASRLNGAPGCVGDEGGELTOKYRNPYSVLLF
DEVEKAPDIFENVLQVLDGILDSRGRKGVDFNSFTIIMTNSLNTALDSDTQVFC
VKGIIHODHOMERKRIIEELRKTYRPFENRIDEVNFHSTODMNPVYKIMQPLIT
TLAEKGTILKIOPLAKHLUSVYGDHMKARLRRTLOTIEDEKLSLIRSLISGH
TLKIGSLGTFPHIA"
/gene="spym18_2135"
/complement(6109..6570)
/gene="spym18_2135"
/complement(6109..6570)
/gene="spym18_2135"
/blastp match gblAAK34730.11 (AE006627)
putative transcriptional regulator [Streptococcus pyogenes
M1 GAS]
/codon_start=1
/transl_table=11
/product="putative transcriptional regulator"
/protein_id="AAL98585.1"
/db_xref="GI:19749201"
/transl_table="MPTKNTSDSIEEYIKELAKSGIAEIKRSLADSPQVPSQIN
YKTRFTESRSGVESKRGSGGVIYRIAKVHSDKHLNGLNLAETECISEQVFTDSI
QLDFDEHLEREGNIILAVASDVLTGDSITIRAMLYRLRLRIDRKGSN"
/complement(6766..6969)
/gene="cspc"
/blastp match gblAAK34730.11 (AE006627)
putative transcriptional regulator [Streptococcus pyogenes
M1 GAS]
/codon_start=1
/transl_table=11
/product="putative cold shock protein"
/protein_id="AAL98586.1"
/db_xref="GI:19749202"
/transl_table="MAGCTVKKMEKGFISTENGDPVAFHSAIOTNGKTLSEB
QKAFDVEGDRGPQAVNITKLA"
/gene="ahpc"
/blastp match gblAAK34730.11 (AE006628)
putative alkyl hydroperoxidase [Streptococcus pyogenes M1
GAS]
/codon_start=1
/transl_table=11
/product="putative alkyl hydroperoxidase"
/protein_id="AAL98587.1"
/db_xref="GI:19749203"
/transl_table="NSLIGKRIAFESAQAHQDKFTYTNDKMGKMAVFCYPADFS
FVCPFTLDLOBYETLKSLGVYSITDTHKAVHSDSVLTITTYPIGDPSH
LISOAFYLDGDELAORFTYDPDGIOMHEINADGIGRDASTLIDKTHAQQYKVKH
PCBYCAKWKCAETLTFPSLDVGKI"
/gene="spym18_2138"
/blastp match gblAAK34730.11 (AE006628)
putative NADH oxidase/alkyl hydroperoxidase reductase
[Streptococcus pyogenes M1 GAS]
/codon_start=1
/transl_table=11
/product="putative NADH oxidase/alkyl hydroperoxidase
reductase"
/protein_id="AAL98588.1"
/db_xref="GI:19749204"
/transl_table="NALSPIKRLQALYLLLEADYLYOVSLENDNOSQKQFVEI
AAMSERISIENTILDRPSFRVAKGKDSQVFRADLPVGHETSLFLALDVSQKAP
VQODYIDIRKAIIDRPIHEFTYVSLTCHNPPVQOLNINSLNDKISHTWEGSMQD
EYKAKGINSYPTVFLDGEPTSGAATLEQLQINGLPSSEAPAKGLYDLVLYGGSP
AGNSAITYAARKGKTGLATFGQVMEVLEIMAGTLYEGKRLAEVKAHTKSY
DVIDIKOILSTIEKENIEVTLNGLAVLOAKTATLALGAKMKNINPGEDEFKNGV
TYCPHCQSPFPEGRDVAIVGGNSGLEALDLAIGLAKRVYVEFLPELAKDKVLODRA
AOTNNTIKRVATKOIVGDHVTGLNTERDSEGRHDLDEGVQIQLVPTATLAK
DSGVNLDRGELLVDHGSTINIPGIFAGDCTDSAYKOIILISWKGATAAIGADYLI

```

```

Query Match          97.8% Score 1602.6; DB 1; Length 11576;
Best Local Similarity 99.1% Pred. No. 0;
Matches 1611; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

gene      RO*
          complement(10126..11412)
          /gene="huti"
          /note="spym18_2139"
          complement(10126..11412)
          /gene="huti"
          /note="Best blastp match sp|P58080|HUTI.STREPY
          HIDA3OLONEPROPIOMASE (IMIDA3OLONE-5-PROPIOMASE
          HYDROLASE)"
          /codon_start=1

CDS
1 ATGCGAAGAAGATCAATTTTCAGCAGATGCGCGTCTGCCATGTCGGCGAGTGAAT
2166 ATGCGAAGAAGATCAATTTTCAGCAGATGCGCGTCTGCCATGTCGGCGAGTGAAT
61 ATGTTAGCAGATACCGCTCAAGTAAAGCTTGTCTCTAAAGGCGCAATGTTCTTGA
2106 ATGTTAGCAGATACCGCTCAAGTAAAGCTTGTCTCTAAAGGCGCAATGTTCTTGA
121 AAAGCTTGTCTCTCTCCCTTAATTAATGAAGGGGTAACATTTGCTTAAGAC
2046 AAAGCTTGTCTCTCTCCCTTAATTAATGAAGGGGTAACATTTGCTTAAGAC
181 TTAGAAGATCATTTGAAAAACATGCGAGCAAAATTTGTCGAATGCTTCAAAAC
1986 TTAGAAGATCATTTGAAAAACATGCGAGCAAAATTTGTCGAATGCTTCAAAAC
241 AATGATATTCCTGATGAGGAGGAGTCAATGATGATGATGATGATGATGATGAT
1926 AATGATATTCCTGATGAGGAGGAGTCAATGATGATGATGATGATGATGATGAT
301 GAAGGATTAATAAATGTCACAGAGTGTCTAATCAATGATGATGATGATGATGAT
1866 GAAGGATTAATAAATGTCACAGAGTGTCTAATCAATGATGATGATGATGATGAT
361 ACAGCAACAGCAACAGCTGTGTAAGGCTTGAAGCCATTGCTCAACCTGATGCAAG
1806 ACAGCAACAGCAACAGCTGTGTAAGGCTTGAAGCCATTGCTCAACCTGATGCAAG
421 GAAGCTATTCCTGATGAGGAGGAGTCAATGATGATGATGATGATGATGATGAT
1746 GAAGCTATTCCTGATGAGGAGGAGTCAATGATGATGATGATGATGATGATGAT
481 TCAGAACATATGAGACGCTGTGAGCAACGATGATGATGATGATGATGATGATGAT
1686 TCAGAACATATGAGACGCTGTGAGCAACGATGATGATGATGATGATGATGATGAT
541 ATGGAACAGCAACGATGAGGAGGAGTGAAGCAATGATGATGATGATGATGATGAT
1626 ATGGAACAGCAACGATGAGGAGGAGTGAAGCAATGATGATGATGATGATGATGAT
601 TACATGCTACAGCAATGAAAAATGTTGCAAGCTTGAAGCAATGATGATGATGAT
1566 TACATGCTACAGCAATGAAAAATGTTGCAAGCTTGAAGCAATGATGATGATGAT
661 ACGGATTAATAAATGTCACAGAGTGTCTAATCAATGATGATGATGATGATGATGAT
1506 ACGGATTAATAAATGTCACAGAGTGTCTAATCAATGATGATGATGATGATGATGAT
721 ACCAACGCTCATCTACTATATTCAGATGATGATGATGATGATGATGATGATGAT
1446 ACCAACGCTCATCTACTATATTCAGATGATGATGATGATGATGATGATGATGAT
781 GTCTTAACAAGATGCTGTGCTTCAATGATGATGATGATGATGATGATGATGATGAT
1386 GTCTTAACAAGATGCTGTGCTTCAATGATGATGATGATGATGATGATGATGATGAT
841 GATCGCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT

```

Wed Apr 16 08:05:37 2003

us-09-001-737-7_copy_15_1652.rge

Db 1326 GATCGCCGCTAAAGCTATGCTTACAGACATTCGATCTGACAGGTGTGACAGTATAC 1267
Qy 901 GAGGATCTAGAGCTTGAATTTAAAGATGCTACATAGACAGCCCTGGACAGGCTCTAAG 960
Db 1266 GAGGATCTAGAGCTTGAATTTAAAGATGCTACATAGACAGCCCTGGACAGGCTCTAAG 1207
Qy 961 ATTACAGTTGATTAAGATAGACACATATTTGAGAGGTGTGAGAGTTCAGAGCTAT 1020
Db 1206 ATTACAGTTGATTAAGATAGACACATATTTGAGAGGTGTGAGAGTTCAGAGCTAT 1147
Qy 1021 GCTAACCGTATGCTGATTAATTCGATTTGAGAGAGTTCAGAGTTCAGAGTTCAGAGT 1080
Db 1146 GCTAACCGTATGCTGATTAATTCGATTTGAGAGAGTTCAGAGTTCAGAGTTCAGAGT 1087
Qy 1081 GAAAAAATCAAGAGAGTTCGAGAAATTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 1140
Db 1086 GAAAAAATCAAGAGAGTTCGAGAAATTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 1027
Qy 1141 GCTCCAGAGAGAGTTCGAGAAATTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 1200
Db 1026 GCTCCAGAGAGAGTTCGAGAAATTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 967
Qy 1201 ACAGCTGACAGCTTCGAGAAATTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 1260
Db 966 ACAGCTGACAGCTTCGAGAAATTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 907
Qy 1261 ATTGAAAAAGTACAGAGCTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 1320
Db 906 ATTGAAAAAGTACAGAGCTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 847
Qy 1321 CTTGCTGCTTACAGAGCTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 1380
Db 846 CTTGCTGCTTACAGAGCTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 787
Qy 1381 GTAGTTATGACAAAGTGAAGAGAGCTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 1440
Db 786 GTAGTTATGACAAAGTGAAGAGAGCTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 727
Qy 1441 GAGTGGGTGATGATTAAGAGAGAGAGCTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 1500
Db 726 GAGTGGGTGATGATTAAGAGAGAGAGCTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 667
Qy 1501 CTTGAAAAATGACAGCTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 1560
Db 666 CTTGAAAAATGACAGCTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 607
Qy 1561 AAACCTGAACAGCTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 1620
Db 606 AAACCTGAACAGCTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 547
Qy 1621 GGTGG 1625
Db 546 GGTGG 542

RESULT 4
LOCUS SPOROELGN 2683 bp DNA linear BCT 26-SEP-1997
DEFINITION S. pyogenes DNA for groEL gene.
ACCESSION X88236.1 GI:2462691
VERSION X88236.1 GI:2462691
KEYWORDS groEL gene; heat shock protein 60 (groEL) like protein.
SOURCE Streptococcus pyogenes
ORGANISM Streptococcus pyogenes
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
REFERENCE 1 (bases 1 to 2683)
AUTHORS Podbielski, A.
TITLE Direct Submission
JOURNAL Submitted (29-JUN-1995) A. Podbielski, Institut f Med
Mikrobiologie, an der Rhein Westf. Techn. Hochschule, Aachen,
Pauwelsstr Klinkum, 52057 Aachen, FRG
* REFERENCE 2 (bases 1 to 2683)
P.

AUTHORS Pohl, B., Podbielski, A. and Zarges, I.
JOURNAL Unpublished
COMMENT Related sequences M81132, M84965.
FEATURES Location/Qualifiers
source 1..2683
/organism="Streptococcus pyogenes"
/strain="serotype M49"
/isolate="CS101"
/db_xref="taxon:1314"
1..1446
/gene="groEL"
<1..1446
/gene="groEL"
/codon_start=1
/trna_table=1
/product="heat shock protein"
/protein_id="CA6150.1"
/db_xref="GI:2462692"
/db_xref="SP:SPRMBL:033733"
/translation="DHFMNKAIVSEVASTNDIAGDGTATATVLTQATVHEGLKNV
TAQANIGIRKIGETATATVAVLAAGPVSREKIAQVAAVSSSEKVEGYISEM
ERYNGDVTTEESRGEHTELEVEGKQFPGRLYSQVATDNEKMAVLEHFLIND
KVSNTQIDILPLEEVKTRPLLIADVDGSLPTLVNKRIGTFNVAVKAPFG
DRKRALEDIAITLGGVITEDGLDNTMTALQAAIKYDQSTVIEGSGSE
ALNARIALKSQLETTSDREKIDREKILAGLAVAYKVGATFETALKEDRIED
ALNARIAVEGIVAGGATLITVEKVALLEBQDAGNITVLALEPVRQIALN
AGGESVVIDLKNKSPAGFMAATGEMVIMITGIDIPVTRISALQMAVSAVSLIL
TTRAVVANKPEPAPAPAPADMDPGWNGF"
1509..1564
repeat_region
/rpl_type="INVERTED
BASE COUNT 808 a 490 c 593 g 792 t
ORIGIN
Query Match 86.3%; Score 1413.4; Db 1; Length 2683;
Best Local Similarity 98.9%; Pred. No. 8.7e-279;
Matches 1423; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Qy 187 GATCATTTTGAAGACATGAGACAAATTTGGTGTGAGAGGCTCTTAAACCAATGAT 246
Db 1 GATCATTTTGAAGACATGAGACAAATTTGGTGTGAGAGGCTCTTAAACCAATGAT 60
Qy 247 ATTGCTGGATGAGAGAGCTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 306
Db 61 ATTGCTGGATGAGAGAGCTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 120
Qy 307 CTTAAAAATGACAGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 366
Db 121 CTTAAAAATGACAGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 180
Qy 367 ACAGACAGCTGTTGAGACCTTGAAGAGCTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 426
Db 181 ACAGACAGCTGTTGAGACCTTGAAGAGCTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 240
Qy 427 ATTGCTGAGTCTGACATATCATCAGCTGTGAGAAAGTGGAGATATATCTGAGA 486
Db 241 ATTGCTGAGTCTGACATATCATCAGCTGTGAGAAAGTGGAGATATATCTGAGA 300
Qy 487 GCTATGAGAGTGTGGCAAGAGATGATGATTAACATCCAGAAATTCGAGATATGAGA 546
Db 301 GCTATGAGAGTGTGGCAAGAGATGATGATTAACATCCAGAAATTCGAGATATGAGA 360
Qy 547 ACAGAACTGAAAGTGTGAGAGATGATGATTAACATCCAGAAATTCGAGATATGAGA 606
Db 361 ACAGAACTGAAAGTGTGAGAGATGATGATTAACATCCAGAAATTCGAGATATGAGA 420
Qy 607 GTACAGACATGAAAAATGTTGAGAGCTTGAAGACCAATTTATCTTAACAGAT 666
Db 421 GTACAGACATGAAAAATGTTGAGAGCTTGAAGACCAATTTATCTTAACAGAT 480
Qy 667 AAAAAAGTCAACATCCAGAGATTTTGCAGTACTTGTAGAGAGTCTTAAACCAAC 726
Db 481 AAAAAAGTCAACATCCAGAGATTTTGCAGTACTTGTAGAGAGTCTTAAACCAAC 540


```

Db 841 GCGATTGCGACTGATTAATTCGCAATTAATAAACAACACTTCTGACTTGAACCGTAAATAA 900
Oy 1087 CTACAGAAGAGCTTTGGCGAAATTAAGCTGGTGTGTAGCTGTTATCAAAAGTAGAGCTTCA 1146
Db 901 CTACAGAAGAGCTTTGGCGAAATTAAGCTGGTGTGTAGCTGTTATCAAAAGTAGAGCTTCA 960
Oy 1147 ACAGAGACAGCTTTAAAGAAATGAATGAACCTTGCATGAGATGCTCTAAATCCACACGT 1206
Db 961 ACAGAGACAGCTTTAAAGAAATGAATGAACCTTGCATGAGATGCTCTAAATCCACACGT 1020
Oy 1207 GCAGCGTTGAAGAGTATGCTGGTGGTGGGAGACAGACTTATACGCTTTTGA 1266
Db 1021 GCAGCGTTGAAGAGTATGCTGGTGGTGGGAGACAGACTTATACGCTTTTGA 1080
Oy 1267 AAGTAGAGCTCTTGAGCTGGAGGGGATGATGCTACTGAGCTAATCAATTGCTGCT 1326
Db 1081 AAGTAGAGCTCTTGAGCTGGAGGGGATGATGCTACTGAGCTAATCAATTGCTGCTG 1140
Oy 1327 GCCTAGAGAGCTCTGAGCTGAATATGCTTAAATGCTGGGTAACAGAGCTCGTAGT 1386
Db 1141 GCCTAGAGAGCTCTGAGCTGAATATGCTTAAATGCTGGGTAACAGAGCTCGTAGT 1200
Oy 1387 ATTGACAAGTGAAGAAACAGCCCTGCAGAGAACGATTTAAATGCTGCAACAGCTGAGT 1446
Db 1201 ATTGACAAGTGAAGAAACAGCCCTGCAGAGAACGATTTAAATGCTGCAACAGCTGAGT 1260
Oy 1447 GTTGATATGATTTAAACAGATATGACCCCTGTCACAAAGTAACAGATCAGCGCTTCA 1506
Db 1261 GTTGATATGATTTAAACAGATATGACCCCTGTCACAAAGTAACAGATCAGCGCTTCA 1320
Oy 1507 AATGACGCTCTGAGCTAGCTGATTTATTTGACAGAGAGAGATGCTGCTTAATTAACCT 1566
Db 1321 AATGACGCTCTGAGCTAGCTGATTTATTTGACAGAGAGAGATGCTGCTTAATTAACCT 1380
Oy 1567 GAACCAAGCTAGCGCAGCGCAAGTCCGACAGAGATGATGATGATGATGATGATGATG 1625
Db 1381 GAACCAAGCTAGCGCAGCGCAAGTCCGACAGAGATGATGATGATGATGATGATGATG 1439

RESULT 6
AY121365 1421 bp DNA linear BCM 30-JUL-2002
LOCUS Streptococcus dysgalactiae subsp. equisimilis strain ATCC 12394
DEFINITION Streptococcus dysgalactiae subsp. equisimilis strain ATCC 12394
ACCESSION AY121365
VERSION AY121365.1 GI:22022489
KEYWORDS
SOURCE Streptococcus dysgalactiae subsp. equisimilis.
ORGANISM Streptococcus dysgalactiae subsp. equisimilis
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
REFERENCE 1 (bases 1 to 1421)
AUTHORS Woo, P.-C. Y., Teng, J. L. L., Lau, S. K. P., Lum, P. N. L., Leung, K. -W.,
TITLE Tse, H., Wong, K. -L., Li, K. -W., Lam, K. -C. and Yuen, K. -Y.
JOURNAL Chapter 11. GroEL gene of Group G Streptococcus dysgalactiae
AUTHORS subsp. equisimilis
TITLE unpublished
JOURNAL 2 (bases 1 to 1421)
AUTHORS Woo, P.-C. Y., Teng, J. L. L., Lau, S. K. P., Lum, P. N. L., Leung, K. -W.,
TITLE Tse, H., Wong, K. -L., Li, K. -W., Lam, K. -C. and Yuen, K. -Y.
JOURNAL Direct Submission
AUTHORS Submitted (12-JUN-2002) Microbiology, The University of Hong Kong,
JOURNAL Pokfulam Road, Hong Kong, China
FEATURES
source
location/Qualifiers
1..1421
/organism="Streptococcus dysgalactiae subsp. equisimilis"
/strain="ATCC 12394"
/sub_species="equisimilis"
/db_xref="ATCC:12394"
/db_xref="taxon:119602"
<1..>1421
/codon_start=3
CDS

```

```

Query Match 71.5%; Score 1170.4; DB 1; Length 1421;
Best Local Similarity 89.0%; Pred. No. 4,6e-229;
Matches 1264; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

Oy 71 ATACCGTCAAAAGTAAAGCTTGTCTTAAAGGGCGCAATGTTCTTGAAGAAAGCTTTG 130
Db 1 ACACGTAAGTAAAGTAAAGCTTGTCTTAAAGGGCGCAATGTTCTTGAAGAAAGCTTTG 60

Oy 131 GTTCTCCCTTAATTAATGACGGGGTAAACCATGCTTAAGATGATGAAATG 150
Db 61 GATCTCCTTGAATTAACCAATGACGGGGTAAACCATGCTTAAGATGATGAAATG 120

Oy 191 ATTTGAAACATGGAGCAAAATGCTGCTGAATGCTTCTTAACCAATGATATG 250
Db 121 ATTTGAAACATGGAGCAAAATGCTGCTGAATGCTTCTTAACCAATGATATG 180

Oy 251 CTGCTGATGGAGCACTACTGACAGATTTTGAACAGCAATGCTTCAATGAAGACTAA 310
Db 181 CAGTGAAGCAAGCAAGTGAACAGATTTTGAACAGCAATGCTTCAATGAAGACTAA 240

Oy 311 AAAATGTGACAGAGTGTATTCATTTGATCCGTCGAGGATGTAAGACAGACAG 370
Db 241 AAAATGTGACAGAGTGTATTCATTTGATCCGTCGAGGATGTAAGACAGACAG 300

Oy 371 CAACAGCTTGAAGCCTTGAAGCCTTGAAGCCTTGAAGCCTTGAAGCCTTGAAGCCTTGA 430
Db 301 CAACAGCCTTGAAGCCTTGAAGCCTTGAAGCCTTGAAGCCTTGAAGCCTTGAAGCCTTGA 360

Oy 431 CTGAGTGGCTGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 490
Db 361 CTGAGTGGCTGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 420

Oy 491 TGAAGCTGTGGCAGACGATGATGATGATGATGATGATGATGATGATGATGATG 550
Db 421 TGAAGCTGTGGCAGACGATGATGATGATGATGATGATGATGATGATGATGATG 480

Oy 551 AACTTGAAGTGTGAAGCATGCAATTTGACCCGTGTTACTGCTCAATACATGCTCA 610
Db 481 AACTTGAAGTGTGAAGCATGCAATTTGACCCGTGTTACTGCTCAATACATGCTCA 540

Oy 611 CAGACAAAGAAAAAATGTTGACGACCTTGAAGAACCAATTAATCTTAACAGATATAA 670
Db 541 CAGACAAAGAAAAAATGTTGACGACCTTGAAGAACCAATTAATCTTAACAGATATAA 600

Oy 671 AAGTGTCAAAAGATCAAGACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 730
Db 601 AAGTGTCAAAAGATCAAGACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660

Oy 731 CATTACTGATTAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 790
Db 661 CATTACTGATTAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 720

Oy 791 AGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 850
Db 721 AGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780

Oy 851 AAGCTTCTTGAAGCATGCTGCTTGAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 910

```

Db 781 AGCTATGCTGAGACATCTCTATCTTGACAGGTGTACAGGATTCACAGATCTAG 840
Qy 911 GACTGATTAAGATGATCTACATGACAGCCCTGGACAGGCTCTAATATACAGTG 970
Db 841 GACTGATTAAGATGATCTACATGACAGCCCTGGACAGGCTCTAATATACAGTG 900
Qy 971 ATAAAGTACACAGTAAATGTTGAGGTTGAGGAGTCTAGACCTTGTCAACCGTA 1030
Db 901 ATAAAGTACACAGTAAATGTTGAGGTTGAGGAGTCTAGACCTTGTCAACCGTA 960
Qy 1031 TTGCAGCTTAATGCAATTTAGAAACAACTGCTGCTTGTACGCTGAAAACATAC 1090
Db 961 TTGCCTGTATGATGATGACACACTGAAACCAACAGCTGATCTTGTACGCTGAAAACATAC 1020
Qy 1091 AAGAGCTTTGGCGAAATTTAGCTGTGTGCTGCTGCTTATCAAGTACAGCTCCACAG 1150
Db 1021 AAGAGCTTTGGCGAAATTTAGCTGTGTGCTGCTGCTTATCAAGTACAGCTCCACAG 1080
Qy 1151 AGACAGCTTTAAAGAAATGAACCTTGCATTTGAGATGCTCTAAATGTCTACAGCTGAG 1210
Db 1081 AAGAGCTTTAAAGAAATGAACCTTGCATTTGAGATGCTCTAAATGTCTACAGCTGAG 1140
Qy 1211 CCGTTGAGAGGATGCTGTGCTGTGTGAGACAGACTTATACGCTATTTGAAAAG 1270
Db 1141 CCGTTGAGAGGATGCTGTGCTGTGTGAGACAGACTTATACGCTATTTGAAAAG 1200
Qy 1271 TAGCAGCTTTGAGGCTGAGGCGATGATGCTAGCTAGCTAATCTTGTGCTGCTC 1330
Db 1201 TAGCAGCTTTGAGGCTGAGGCGATGATGCTAGCTAATCTTGTGCTGCTC 1260
Qy 1331 TAGCAGCTTTGAGGCTGAGGCGATGATGCTAGCTAATCTTGTGCTGCTC 1390
Db 1261 TAGCAGCTTTGAGGCTGAGGCGATGATGCTAGCTAATCTTGTGCTGCTC 1320
Qy 1391 ACAAGTGAAGAAAGAGGCTGAGGAGAAAGATTTAATCTGCAACAGGTGAGTGTTG 1450
Db 1321 ACAAGTGAAGAAAGAGGCTGAGGAGAAAGATTTAATCTGCAACAGGTGAGTGTTG 1380
Qy 1451 ATATGATTAAGAAAGAGGATGATGCTGCTGCAAGTAAC 1490
Db 1381 ATATGATTAAGAAAGAGGATGATGCTGCTGCAAGTAAC 1420

RESULT 7
AX148806 1306 bp DNA linear PAT 08-JUN-2001
LOCUS AX148806
DEFINITION Sequence 8 from Patent WO0136625.
ACCESSION AX148806
VERSION AX148806.1 GI:14347330
KEYWORDS
SOURCE Streptococcus pyogenes.
ORGANISM Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
REFERENCE 1 (bases 1 to 1306)
AUTHORS Wright,J.A., Young,A.H. and Dugourd,D.
TITLE Inhibitors of nucleotide sequences derived from groEL and groES as
inhibitors of streptococcal growth.
JOURNAL Patent: WO 0136625 A 8 25-MAY-2001;
Genesense Technologies Inc. (CA)
FEATURES
Location/Qualifiers
1..1306
/organism="Streptococcus pyogenes"
/db_xref="taxon:1314"
BASE COUNT 407 a 235 c 308 g 356 t
ORIGIN

Query Match 69.6%; Score 1140.4; DB 6; Length 1306;
Best Local Similarity 99.9%; Pred. No. 6.3e-223;
Matches 1141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 484 GAAGCTATGAGCGTGTGGCAAGATGCTGATTAACATCAAGATCTCGAGTATG 543

Db 2 GAAGCTATGAGCGTGTGGCAAGATGCTGATTAACATCAAGATCTCGAGTATG 61
Qy 544 GAACAGAACTTGAAGTGTGAGAGCAATTTGACCGTGTATACCTGTCTCAATAC 603
Db 62 GAACAGAACTTGAAGTGTGAGAGCAATTTGACCGTGTATACCTGTCTCAATAC 121
Qy 604 ATGTGACAGCAATGAAGAAATGTTGACAGCTTGAAGAACCATTTATCTAATACG 663
Db 122 ATGTGACAGCAATGAAGAAATGTTGACAGCTTGAAGAACCATTTATCTAATACG 181
Qy 664 GATAAAGAGTGTCAACATCCAGACATTTTGCACACTTGTGAGAAATGCTTAAACG 723
Db 182 GATAAAGAGTGTCAACATCCAGACATTTTGCACACTTGTGAGAAATGCTTAAACG 241
Qy 724 AACGCTCATTAATTTGACAGATGATGATGATGATGATGATGATGATGATGATGATG 783
Db 242 AACGCTCATTAATTTGACAGATGATGATGATGATGATGATGATGATGATGATGATG 301
Qy 784 TTGACAGAAATGCTGTGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843
Db 302 TTGACAGAAATGCTGTGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361
Qy 844 CCGTGAAGCTATGCTTGAAGACATTTGCTATCTTGAAGAGTGTACAGTATTAACAG 903
Db 362 CCGTGAAGCTATGCTTGAAGACATTTGCTATCTTGAAGAGTGTACAGTATTAACAG 421
Qy 904 GATCTAGAGCTTAATTAAGATGCTACAAATGACAGCCCTTGAAGAGCTGTAAGAT 963
Db 422 GATCTAGAGCTTAATTAAGATGCTACAAATGACAGCCCTTGAAGAGCTGTAAGAT 481
Qy 964 ACAGTGAATGAAGATGACAGATTAATTTGTAAGGTTGAGAAAGTTGAAAGATTTGT 1023
Db 482 ACAGTGAATGAAGATGACAGATTAATTTGTAAGGTTGAGAAAGTTGAAAGATTTGT 541
Qy 1024 AACGCTATTAATTAATTAATGCAATTAAGAAACAACTTGTGATTTGACCTGAA 1083
Db 542 AACGCTATTAATTAATTAATGCAATTAAGAAACAACTTGTGATTTGACCTGAA 601
Qy 1084 AAACGATTAAGAGTGTGGGAAATAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1143
Db 602 AAACGATTAAGAGTGTGGGAAATAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 661
Qy 1144 CCACAGAGAGCTTTAAAGAAATGAATGCAATTTGCTGATGAGATGCTTAAATGCTACA 1203
Db 662 CCACAGAGAGCTTTAAAGAAATGAATGCAATTTGCTGATGAGATGCTTAAATGCTACA 721
Qy 1204 GGTGACAGCGTTGAAGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1263
Db 722 GGTGACAGCGTTGAAGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 781
Qy 1264 GAAAAGTACAGCTCTTGAGCTTGAGGCGATGATGCTAGTACGTAACATTTGCTG 1323
Db 782 GAAAAGTACAGCTCTTGAGCTTGAGGCGATGATGCTAGTACGTAACATTTGCTG 841
Qy 1324 CGTCTCTGTAAGAGCGCTGTAAGTCAATTTGCTTAAATGCTGCTGCTGCTGCTGCTG 1383
Db 842 CGTCTCTGTAAGAGCGCTGTAAGTCAATTTGCTTAAATGCTGCTGCTGCTGCTGCTG 901
Qy 1384 GTTATGTAAGATTTGAAGAAACAGCCCTGACAGAAAGATTTAATGCTGCAACAGTAG 1443
Db 902 GTTATGTAAGATTTGAAGAAACAGCCCTGACAGAAAGATTTAATGCTGCAACAGTAG 961
Qy 1444 TGGGTGATGATTTAAACAGGAATCATTTGACCTGCTCAAGATTAACAGATCAGCGTT 1503
Db 962 TGGGTGATGATTTAAACAGGAATCATTTGACCTGCTCAAGATTAACAGATCAGCGTT 1021
Qy 1504 CAAATGACGCTTGTGATGATGCTTATTTTGAACAGAAAGAGTGTGCTTAATTA 1563
Db 1022 CAAATGACGCTTGTGATGATGCTTATTTTGAACAGAAAGAGTGTGCTTAATTA 1081
Qy 1564 CTTGAACAGCTTACAGCGCAGCAATCCAGCAGGATGATGATCCAGAAATGATGGT 1623

Db 1082 CCGTGAACAGTACGACCGCCGCGCAATGCGACAGCATGTGATCCAGATGATGAGGC 1141
 Oy 1624 GG 1625
 Db 1142 GG 1143

RESULT 8
 AY121364
 LOCUS AY121364
 DEFINITION Streptococcus dysgalactiae subsp. equisimilis strain ATCC 35666
 ACCESSION AY121364
 VERSION AY121364.1 GI:22022487
 KEYWORDS
 SOURCE Streptococcus dysgalactiae subsp. equisimilis.
 ORGANISM Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 Streptococcus.
 REFERENCE 1 (bases 1 to 1421)
 Moo, P.C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W.,
 Tse, H., Mong, K.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.,
 Chapterin GroEL gene of Group C Streptococcus dysgalactiae
 subsp. equisimilis
 TITLE Unpublished
 JOURNAL 2 (bases 1 to 1421)
 REFERENCE Moo, P.C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W.,
 Tse, H., Mong, K.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.,
 Direct Submission
 JOURNAL Submitted (12-JUN-2002) Microbiology, The University of Hong Kong,
 Pokfulam Road, Hong Kong, China
 FEATURES
 source
 1. 1421
 Location/Qualifiers
 /organism="Streptococcus dysgalactiae subsp. equisimilis"
 /strain="ATCC 35666"
 /sub-species="equisimilis"
 /db_xref="ATCC:35666"
 /db_xref="taxon:119602"
 <1..>1421
 /codon_start=3
 /transl_table=11
 /product="Chapterin GroEL"
 /protein_id="FAM83127.1"
 /db_xref="GI:22022487"
 /translation="VTLSPEKRNVLLEKRGSPITNDGVTAKIELEHDFENMGAK
 LYSPEAKRTNDINGGTTATVLOAVREGSLKNTVGANPVGIRGLETATAVEA
 LKAIADYVSKREHIAQVAASVSSEKVEFISEMERVNDGVTIEESRMELEVE
 VEGMDFRGTLISQVWTDNEKNVADLENFLLIDDKVSNIDVILPLEEVLKTNPL
 LTIADVDGALPITVLRKIRGTFNVAVKARFGDGDRKMLIEDIALITGVTITEDL
 GLESLKALPMLGSAKATYVDKSTVYVKGASSEAIANKMLIEDIALITGVTITEDL
 KLSRLAKLGGAVAIKVGATKELRIEDALNATRAAVEGVVAGGCTALIT
 VIERVALELDDBDADGNTIVLRALDEEPRVRIANNAVEGSLVLDKLNPSVGTGNA
 ATGEMVMDIAGIIDPVVTRSA"

BASE COUNT 408 a 275 c 354 g 384 t
 ORIGIN

Query Match 68.9%; Score 1128.8; DB 1; Length 1421;
 Best Local Similarity 87.2%; Pred. No. 1.5e-220;
 Matches 1238; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

Oy 80 AAGTAAGCGTGTGCTTAAGGCGCAATGTTGCTTGAAGAAAGCTTTGGTCCCT 139
 Db 1 AAGTAAGCGTGTGCTTAAAGCTGTAAGCGTGTGCTTGAAGAAAGCTTTGGTCCCT 60

Oy 140 TAATTAATTAAGAGCGGTACCATTTGCTAAAGATGCAATTAAGATCATTTTGAAA 199
 Db 61 TGATTACCATGACGGGTTACCATTTGCTAAAGAGATGCAATTAAGATCATTTTGAGA 120

Oy 200 ACATGAGCAAAATTTGCTGTAAGTGGCTTCTAAACCAATGATATTGGTGATG 259
 Db 121 ATATGGAGCTAAATTTGCTTTCGAAGTGGCTTCTAAACCAATGATATTGGTGATG 180

Oy 260 GGAAGCACTACTGCAACAGTTTGGACCAAGCATTTGCTGTAAGAGCATTAAGATGCA 319

Db 181 GAAACCAACTGCAACAGTATTTGACACAGCGTATCGCTGTAAAGGCTTAAAAATGTA 240
 Oy 320 CAGCAGGTGCTATTCATTTGCTATCGCTGCGAGCATTTGAAACAGCAACAGCATG 379
 Db 241 CTGCTGTGCGCAACCAATTTGCTATTCGCTGCGAGTATGAAACAGCAACAGCGC 300
 Oy 380 TTGAAGCTTGAAGCAATTTGCTATTCGCTATTTGCGAAGAGCATTTGCTGATG 439
 Db 301 TTGAAGCTTGAAGCAATTTGCTATTCGCTATTTGCGAAGAGCATTTGCTGATG 360
 Oy 440 CTGCAATGATCATCGCTGTGAAAGAGTATGATCTGCAAGAGCATTTGAGCGTG 499
 Db 361 CTGCTGTGCTATTCGCTGTGAAAGAGTATGATCTGCAAGAGCATTTGAGCGTG 420
 Oy 500 TGCGCAACGATGTGTGATTTACATGAAAGATCTGAGATGTAAGAAAGCATTTGAG 559
 Db 421 TGCGCAACGATGTGTGATTTACATGAAAGATCTGAGATGTAAGAAAGCATTTGAG 480
 Oy 560 TGCTGAGGCAATGATTTGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 619
 Db 481 TGCTGAGGCAATGATTTGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 Oy 620 AAAAAATGCTGAGACCTTGAAGCAACCATTTATCTATTCAGCATTAAGATGCTGA 679
 Db 541 AAAAAATGCTGAGACCTTGAAGCAACCATTTATCTGATTTGAGCAAGATGCTGA 600
 Oy 680 ACATCCAGACATTTTGGCCACTTCTGAGAGATTTTAAACCAACCGTCCATTACTCA 739
 Db 601 ACATCCAGACATTTTCCACTTCTGAGAGATTTTAAACCAACCGTCCATTACTCA 660
 Oy 740 TTATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 799
 Db 661 TTATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 Oy 800 GTACCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 859
 Db 721 GTACCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 Oy 860 TTGAACATGCTATTTGAGAGGCTGATGATGATGATGATGATGATGATGATGAT 919
 Db 781 TTGAACATGCTATTTGAGAGGCTGATGATGATGATGATGATGATGATGATGAT 840
 Oy 920 TAAAGATGCTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 979
 Db 841 TGAAGATGCTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 Oy 980 GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1039
 Db 901 GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 Oy 1040 TTAATTCGATTTGAAGCAACCACTTGTGATGATGATGATGATGATGATGAT 1099
 Db 961 TTAATTCGATTTGAAGCAACCACTTGTGATGATGATGATGATGATGATGAT 1020
 Oy 1100 TGCGCAACGATGTGTGATTTACATGAAAGATCTGAGATGTAAGAAAGCATTTGAG 1159
 Db 1021 TGCGCAACGATGTGTGATTTACATGAAAGATCTGAGATGTAAGAAAGCATTTGAG 1080
 Oy 1160 TAAAGAAATGAAGCACTTGCATGAGATGCTCTAAAGTCAAGTGCACCGCTGAAG 1219
 Db 1081 TTAAGAAATGAAGCACTTGCATGAGATGCTCTAAAGTCAAGTGCACCGCTGAAG 1140
 Oy 1220 AAGTATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1279
 Db 1141 AAGTATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 Oy 1280 TTGAGCTTGAAGCAATTTGCTGATGATGATGATGATGATGATGATGATGATGAT 1339
 Db 1201 TTGAGCTTGAAGCAATTTGCTGATGATGATGATGATGATGATGATGATGATGAT 1260
 Oy 1340 CTGTAAGCAATTTGCTTAAAGTGTGAGTGAAGGCTCCGTAATTTGAGCAAGTGA 1399

DB	1261	CTTTCGCAAAATGCATTCACACCTGGTTAGCAAGTCCGTTGTATTCAGCAAAATGTA	1320
Oy	1400	AAACACAGCCCTGCAGAGACACAGATTTAAATGCGACAGAGTGAGGCGGTGATATATATA	1459
Db	1321	AAAAATAGCCCTGTTGGACACAGCTTTAAATGCGACAGAGTGAATGAGTATATATG	1380
Oy	1460	AAACGAGAAATCATTCAGCCCTCCTCAAGCTATACAGCATAGC	1499
Db	1381	CGCAGCATTTATTCATCTCTTAAAGTAAACCCGTCAGC	1420

FEATURES	source
REFERENCE	1. 1422 /organism="Streptococcus dysgalactiae subsp. equisimilis" /strain="Cip 55-123" /sub_species="equisimilis" /db_xref="taxon:119602"
TITLE	<1>1422 /codon_start=1 /transl_table=11 /product="Chaperonin GroEL" /protein_id="AA081129.1" /db_xref="GI:22022491"
JOURNAL	/translation="kVYLGRKNNVLEKAFGSPILITDGYITAKIELEDEHFNKMGAKLVEVASTKINDIAGDDGTATVLTQATVRGKNTVACAPDIDIRGLETATAVEALAKRAIVASGKEALDAQAAVASSRSRKEGVEISENAREGNDGYITIEBSRGMETEELVBSMDGDEGTLPTVNTDNEKKNVADLENPELITITPKKXSNIDILPELVEYLTNNP
AUTHORS	1. (bases 1 to 1422) Woo, P.C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W., Tse, H., Wong, K.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.
CHAPERONIN GROEL	Chaperonin GroEL gene of Group I Streptococcus dysgalactiae subspecies equisimilis
UNPUBLISHED	2 (bases 1 to 1422) Woo, P.C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W., Tse, H., Wong, K.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.
LOCUS	AA081129.1
DEFINITION	Streptococcus dysgalactiae subsp. equisimilis strain Cip 55-123
ACCESSION	AF121366.1
VERSION	GI:22022491
KEYWORDS	Streptococcus, Firmicutes, Lactobacillales, Streptococcaceae, Streptococcus.
ORGANISM	Streptococcus dysgalactiae subsp. equisimilis.
REFERENCE	1. (bases 1 to 1422) Woo, P.C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W., Tse, H., Wong, K.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.
TITLE	Chaperonin GroEL gene of Group I Streptococcus dysgalactiae subspecies equisimilis
JOURNAL	Submitted (12-JUN-2002) Microbiology, The University of Hong Kong, Pokfulam Road, Hong Kong, China
AUTHORS	1. 1422 /organism="Streptococcus dysgalactiae subsp. equisimilis" /strain="Cip 55-123" /sub_species="equisimilis" /db_xref="taxon:119602"
TITLE	<1>1422 /codon_start=1 /transl_table=11 /product="Chaperonin GroEL" /protein_id="AA081129.1" /db_xref="GI:22022491"
CHAPERONIN GROEL	Chaperonin GroEL gene of Group I Streptococcus dysgalactiae subspecies equisimilis
UNPUBLISHED	2 (bases 1 to 1422) Woo, P.C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W., Tse, H., Wong, K.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.
LOCUS	AA081129.1
DEFINITION	Streptococcus dysgalactiae subsp. equisimilis strain Cip 55-123
ACCESSION	AF121366.1
VERSION	GI:22022491
KEYWORDS	Streptococcus, Firmicutes, Lactobacillales, Streptococcaceae, Streptococcus.
ORGANISM	Streptococcus dysgalactiae subsp. equisimilis.
REFERENCE	1. (bases 1 to 1422) Woo, P.C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W., Tse, H., Wong, K.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.
TITLE	Chaperonin GroEL gene of Group I Streptococcus dysgalactiae subspecies equisimilis
JOURNAL	Submitted (12-JUN-2002) Microbiology, The University of Hong Kong, Pokfulam Road, Hong Kong, China
AUTHORS	1. 1422 /organism="Streptococcus dysgalactiae subsp. equisimilis" /strain="Cip 55-123" /sub_species="equisimilis" /db_xref="taxon:119602"
TITLE	<1>1422 /codon_start=1 /transl_table=11 /product="Chaperonin GroEL" /protein_id="AA081129.1" /db_xref="GI:22022491"
CHAPERONIN GROEL	Chaperonin GroEL gene of Group I Streptococcus dysgalactiae subspecies equisimilis
UNPUBLISHED	2 (bases 1 to 1422) Woo, P.C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W., Tse, H., Wong, K.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.
LOCUS	AA081129.1
DEFINITION	Streptococcus dysgalactiae subsp. equisimilis strain Cip 55-123
ACCESSION	AF121366.1
VERSION	GI:22022491
KEYWORDS	Streptococcus, Firmicutes, Lactobacillales, Streptococcaceae, Streptococcus.
ORGANISM	Streptococcus dysgalactiae subsp. equisimilis.
REFERENCE	1. (bases 1 to 1422) Woo, P.C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W., Tse, H., Wong, K.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.
TITLE	Chaperonin GroEL gene of Group I Streptococcus dysgalactiae subspecies equisimilis
JOURNAL	Submitted (12-JUN-2002) Microbiology, The University of Hong Kong, Pokfulam Road, Hong Kong, China
AUTHORS	1. 1422 /organism="Streptococcus dysgalactiae subsp. equisimilis" /strain="Cip 55-123" /sub_species="equisimilis" /db_xref="taxon:119602"
TITLE	<1>1422 /codon_start=1 /transl_table=11 /product="Chaperonin GroEL" /protein_id="AA081129.1" /db_xref="GI:22022491"
CHAPERONIN GROEL	Chaperonin GroEL gene of Group I Streptococcus dysgalactiae subspecies equisimilis
UNPUBLISHED	2 (bases 1 to 1422) Woo, P.C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W., Tse, H., Wong, K.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.
LOCUS	AA081129.1
DEFINITION	Streptococcus dysgalactiae subsp. equisimilis strain Cip 55-123
ACCESSION	AF121366.1
VERSION	GI:22022491
KEYWORDS	Streptococcus, Firmicutes, Lactobacillales, Streptococcaceae, Streptococcus.
ORGANISM	Streptococcus dysgalactiae subsp. equisimilis.
REFERENCE	1. (bases 1 to 1422) Woo, P.C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W., Tse, H., Wong, K.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.
TITLE	Chaperonin GroEL gene of Group I Streptococcus dysgalactiae subspecies equisimilis
JOURNAL	Submitted (12-JUN-2002) Microbiology, The University of Hong Kong, Pokfulam Road, Hong Kong, China
AUTHORS	1. 1422 /organism="Streptococcus dysgalactiae subsp. equisimilis" /strain="Cip 55-123" /sub_species="equisimilis" /db_xref="taxon:119602"
TITLE	<1>1422 /codon_start=1 /transl_table=11 /product="Chaperonin GroEL" /protein_id="AA081129.1" /db_xref="GI:22022491"
CHAPERONIN GROEL	Chaperonin GroEL gene of Group I Streptococcus dysgalactiae subspecies equisimilis
UNPUBLISHED	2 (bases 1 to 1422) Woo, P.C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W., Tse, H., Wong, K.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.
LOCUS	AA081129.1
DEFINITION	Streptococcus dysgalactiae subsp. equisimilis strain Cip 55-123
ACCESSION	AF121366.1
VERSION	GI:22022491
KEYWORDS	

Dp	121	AAATGGGAGCTAAATTGGTTCTGAAAGTTGCTCTCAAAACCAATGATTCGACAGTGAC	180
Oy	259	GGAGACGACTACTGCAACACTTTTGTGCAACAAACCATGTTCTCATGAAGCTATAAAATGTG	318
Dp	181	GGAACCCAACTGACACACTATATGACACAGCACTATCTGCTGTAAAGGCTTAAAAATGTA	240
Oy	319	ACACAGCGTGTAAATTCATTTGTRTCCGTGAGCACTTGAACGACACACACAGCT	378
Dp	241	ACTGCGGTGGCAACCCAAATGTGTAATTCGTGCTGGGATTTGAACAGCAACACAAACGCC	300
Oy	379	GTTGAGCGCTTGAAGCCATTGGCTCAACCTGTATCTGCGACAGAAAGCTATTGCTCAGTGC	438
Dp	301	GTTGAAGCGCTTGAAGAACTTTGCTCTCAGCCCTGTTCTGGTAAAGAGGATTCCTCAAGTT	360
Oy	439	GCTGCAGTATCATCAGCTCTGTAAGAAAGTTGAGAGATATATCTCAGAACCTATGAGACGT	498
Dp	361	GGCTGTGTGTATCTGTTCTGTGAAAAAGTTGGAGAAATCATCTCTACAAACCTGGAACGT	420
Oy	499	GTTGGCAACGATGGTGTGATTTACCATGAGAAATCTCAGAGTATGAAACACAACTTGAA	558
Dp	421	GTTGGCAATGACGGTGTCAATTCATGTGAAGAAATCAGCTGGTATGGAGACACACTTGAA	480
Oy	559	GTTGGTGAAGCAATGCAATTTGACCCGTGGTACCTGTCTCAATTCATGGTCCAGACAAAT	618
Dp	481	GTTGTAGAAGGCATACGAGTTTGACCGTGTACTGTCTCAATTCATGGTCCAGACAAAT	540
Oy	619	GAAAAATGTTGACACCTTGAAAAACCCATTATCTTAATCAGAGATAAAAAGTGTCTC	678
Dp	541	GAAAAATGTTGACACCTTGAAAAACCCATTATCTTAATCAGAGATAAAAAGTGTCTC	600
Oy	679	AACATCCAAAGCAATTTGGCACTACTGAGAGAAAGTCTTAAACAAACCGTCAATATCTC	738
Dp	601	AACATCCAAAGTATTTCCCATTTACTTGAAGAAAGTCTTAAACAAACCGTCAATATCTC	660
Oy	739	ATTATGTAGATATGTGATGATGAGGAAGCAATTTCCAAACCTTGTCTTAAACAATATCGT	798
Dp	661	ATTATGCGCCATGACCTTGAAGCGAAAGCTTCCAAACCTTGTCTTGAATTAATATCGT	720
Oy	799	GGTACTTTCATATGTTGTGTCTGTCTAAAGCGCAAGATTTGGTGTATCTGTCTGAAGATATG	858
Dp	721	GGTACTTTCATATGTTGTGTCTGTCTAAAGCGCTCCAGGATTTGGTGTATCTGTCTGAAGATATG	780
Oy	859	CTTGAAGCAATGCTATCTCTTGAACAGGTGTGACAGATTTACAGAGGATCTAGACACTTGAA	918
Dp	781	CTTGAAGCAATGCTCTTCTTGAACAGGTGTGACAGATTTACAGAGGATCTAGACACTTGAA	840
Oy	919	TTAAAGATGCTCTCAATGACAGCCCTTGGACAGCGTGTCTAAAGATTTACAGTGTATTAAGAT	978
Dp	841	TTGAAGAGCCCTCAATGACAGCTCTTGGACAGCCCGTAAATGACTGTGTGATTAAGAC	900
Oy	979	ACACAGCAATTTTGAAGGTCTCAGAGAGTCTCAGAGGTATTTCTTACCGTATATGACAG	1038
Dp	901	ACACAGCTTTTGTGGAAGGTGACAGAAAGTCTGAAGCATCTCCAAACCGTGTGGGTG	960
Oy	1039	ATTAAATGCAATTTGAAGCAACAAACCTCTGACTTTGACCGTAAACCTCAAGAAAGCT	1098
Dp	961	ATTAAATGCAATTTGAAGCAACCAACAGCTGTGACTTTGACCGTAAATTTCAATGAAAGC	1020
Oy	1099	TTGGCGAAATTTACCGTGGGTGTACGCTTATCAAAATGAGAGCTCCAAACAGACAGCT	1158
Dp	1021	TTGGCGAAATTTACCTGT	1080
Oy	1159	TTAAAGCAATTTGAACCTTCCATTTGAGATGCTCTAAATGCTTCAACGTGACAGCGCTTGA	1218
Dp	1081	CTTAAGCAATTTGAACCTTCTGTATGCAAGATGCTCTGAATCTCCAAACGTGACAGCTTGTGA	1140
Oy	1219	GAAAGTATGCTGTGCTGTGTGTGGAACAGCACTTTATACGGTTATTTGAAAAAAGTAGACGT	1278
Dp	1141	GAAAGTATGCTGTGCTGTGTGTGGAACAGCACTTTATACGGTGTGAAAAAAGTAGCTGT	1200
Oy	1279	CTTAGAGCTTAGAGGGAGATGATGCTACTGACAGCTAAATTTGTGCTTGTGTGCTTAGAAGAG	1338
Dp	1201	CTTAGAGCTTAGAGGGAGATGATGCTACTGACAGCTAAATTTGTGCTTGTGTGCTTAGAAGAG	1260

1339 CCTGTAGTCATCAATTTGCTTTAAATGCTGGGTAGCAGGCTCCGTAGTATTATGACAGTTC 1398
1261 CTTGTCGTCATTAATGATTCATCAACGCTGGTTATCAAGAGTTCCTGTCATCAACATTTG 1320
1339 AAAAAGCCCTGCGAGAGACAGATTTAATGCTCAACAGAGTGAATGGTTCATATGATT 1458
1331 AAAAATAGCCCTGTTGGAACAGCTTTAATGCGCAACAGAGTGAATGGTGAATATGATT 1380
1459 AAAACGAGATCATTTGACCTCTCAACATGACAGCATGAC 1499
1381 GCGGCGATTTATGATCCTGTTAAAGTAAACCGCTTCAGC 1421

RESULT 10
AX148809 1305 bp DNA Linear PAT 08-JUN-2001
LOCUS AX148809 Sequence 11 from Patent M00136625.
ACCESSION AX148809
VERSION AX148809.1 GI:14347333
KEYWORDS
SOURCE Streptococcus pyogenes.
ORGANISM Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.

REFERENCE 1 (bases 1 to 1305)
AUTHORS Wright, J. A., Young, A. H. and Dugourd, D.
TITLE Antisense oligonucleotide sequences derived from groEL and groES as
inhibitors of microorganisms
Patent: WO 0136625-A1 25-MAY-2001;
JOURNAL Genesense Technologies Inc. (CA)
FEATURES
source location/Qualifiers
1..1305
/organism="Streptococcus pyogenes"
/db_xref="taxon:1314"
BASE COUNT 406 a 238 c 312 g 349 t
ORIGIN

Query Match 68.5%; Score 1122.6; DB 6; Length 1305;
Best Local Similarity 99.2%; Pred. No. 2,7e-219;
Matches 1128; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

969 TGATTAAGATGACACAGTATTTGTTGAAGGTCAGAGAGTTCCAGAACTATTGCTAACCG 1028
481 TGATTAAGATGACACAGTATTTGTTGAAGGTCAGAGAGTTCCAGAACTATTGCTAACCG 540
1029 TATTCAGCTATTAATTCGCAATTAGAACACAACTTGTGACTTGAACCTGAAAAACT 1088
541 TATTCAGCTATTAATTCGCAATTAGAACACAACTTGTGACTTGAACCTGAAAAACT 600
1089 ACAGAACGTTTGGCAATTAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1148
601 ACAGAACGTTTGGCAATTAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 660
1149 AGAGACAGCTTTAAAGAAATGAATGCAATGAGATGAGATGAGATGAGATGAGATGAGAT 1208
661 AGAGACAGCTTTAAAGAAATGAATGCAATGAGATGAGATGAGATGAGATGAGATGAGAT 720
1209 AGCGGTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1268
721 AGCGGTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
1269 AGTACAGCTTGTGACCTTGAGGCGCATGATGATGATGATGATGATGATGATGATGATGAT 1328
781 AGTACAGCTTGTGACCTTGAGGCGCATGATGATGATGATGATGATGATGATGATGATGAT 840
1329 TCTAGAACAGCTGTACGTAATGCTTTAAATGCTGAGGATGAGAGCTCCGATGATT 1388
841 TCTAGAACAGCTGTACGTAATGCTTTAAATGCTGAGGATGAGAGCTCCGATGATT 900
1389 TGACAAAGTTAAACAGACCCCTGCAGAACAGATTTAATGCTGCAACAGGATGAGGAT 1448
901 TGACAAAGTTAAACAGACCCCTGCAGAACAGATTTAATGCTGCAACAGGATGAGGAT 960
1449 TGATATGATTTAAACAGACATGATGACCTGCAAGATGACATGACATGACATGACATGACAT 1508
961 TGATATGATTTAAACAGACATGATGACCTGCAAGATGACATGACATGACATGACATGACAT 1020
1509 TGCACCTTGTGTAGTACGTTATTTTGAACAGAGAGGTTGTGTAATTAACCTGA 1568
1021 TGCACCTTGTGTAGTACGTTATTTTGAACAGAGAGGTTGTGTAATTAACCTGA 1080
1569 ACCACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1635
1081 ACCACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1137

RESULT 11
AY121367 1415 bp DNA Linear BCT 30-JUL-2002
LOCUS AY121367 Streptococcus dysgalactiae strain HKU 7, chaperonin GroEL gene,
partial cds.
ACCESSION AY121367
VERSION AY121367.1 GI:22022493
KEYWORDS
SOURCE Streptococcus dysgalactiae.
ORGANISM Streptococcus dysgalactiae.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.

REFERENCE 1 (bases 1 to 1415)
AUTHORS Moo, P. C. Y., Teng, J. L. L., Lau, S. K. P., Lum, P. N. L., Leung, K. W.,
Tse, H., Wong, K. L., Li, K. W., Lam, K. C. and Yuen, K. Y.
TITLE Chaperonin GroEL gene of Group G Streptococcus dysgalactiae
unpublished
JOURNAL Moo, P. C. Y., Teng, J. L. L., Lau, S. K. P., Lum, P. N. L., Leung, K. W.,
Tse, H., Wong, K. L., Li, K. W., Lam, K. C. and Yuen, K. Y.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Microbiology, The University of Hong Kong,
Pokfulam Road, Hong Kong, China
FEATURES
source location/Qualifiers
1..1415
/organism="Streptococcus dysgalactiae"
/strain="HKU 7"

```

CDS
/db_xref="taxon:1334"
<1..21415
/codon_start=3
/terminal_table=11
/product="chaperonin GroEL"
/protein_id="A083130.1"
/db_xref="GI:22022484"
/translation="LGRGRNVYLKAGSPILTDNGVTIAKEIELEDFHEKAKLV
SEVASTNDIADGGTTATVLTALVREGLANVTAQANITGRITGTAFAVAALV
ALADPVSKEATIAQVAAYVSSRSKERTISAMRNGVNGITTEESRGKTELEVE
IMODPRTLSOIMTDEKRYADLNPILITLTKRVSNIODITLLEVLKTNRLI
IADVDGEALPTVLNKIRGTENVVAAPEDDRKASLIDILGGLVITLEDGL
ELKDATPAPLGAQAKVVDQSTVLEBAGSSSAIANRGLIKQLSTTSFDEKL
EKVALELDGDADGRNI VLRALESPVQIIFNAGESVVIDLRKNSPVGTGFAAT
GEWDMIAAGIIDPVKYNRSA"
BASE COUNT      404 a 276 c 353 g 382 t
ORIGIN
Query Match      68.3%; Score 1118; DB 1; Length 1415;
Best Local Similarity 86.9%; Pred. No. 2,3e-218;
Matches 1229; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

OY 86 CGCTGGTCTTAAAGGCGCAATGTTCTTGAAGAAAGCTTTGGTCCCTTAATA 145
DB 1 CGCTGGTCTTAAAGGCGCAATGTTCTTGAAGAAAGCTTTGGTCCCTTAATA 60
OY 146 CTATAGCGGGTAAACCATTTGCTTAAAGATCGAATTAGAACATCTTTGAAAACATGG 205
DB 61 CCAATGACGGGTTACCATTTGCTTAAAGATCGAATTAGAACATCTTTGAAAACATGG 120
OY 206 GAGCAAAATGGTGTGGAAGGCTTCTTAAACCAATGATATTGCTGGTATGGAGCA 265
DB 121 GACCTAAATGGTGTGGAAGGCTTCTTAAACCAATGATATTGCTGGTATGGAGCA 180
OY 266 CTATGCAAGTTTGTGACACAGCATTTGTCATGAGAGCATTTAAATAATGACAGAG 325
DB 181 CAATGCAAGTTTGTGACACAGCATTTGTCATGAGAGCATTTAAATAATGACAGAG 240
OY 326 GTGCTAATCATTTGTTATCCGTCGAGGCAATGAAACAGCAACAGCAAGCTGTAG 385
DB 241 GTGCAACCAATTTGTTATCCGTCGAGGCAATGAAACAGCAACAGCAAGCTGTAG 300
OY 386 CTTGAAAGCAATGCTCAACCTGTATCTGGCAAGAACTATTGCTCAGGCTGCGAG 445
DB 301 CTTGAAAGCAATTTGCTCAGGCTGTGTTGTAAGAAAGCAATTTGCTCAGGCTG 360
OY 446 TATCATACGCTGTGAAAAAGTTGAGAGTATCTCAGAAAGCTATGAGCGCTGGGCA 505
DB 361 TGTCACTCTGCTTGAAGAAAGTTGAGAGTATCTCAGAAAGCTATGAGCGTGGGCA 420
OY 506 ACGATGGTGTATACCATCGAAGATCTCGAGGTATGAAACGAACCTTGAAAGGTG 565
DB 421 ATGACGGTGTATACCATCGAAGATCTCGAGGTATGAAACGAAGCTTGAAAGGTG 480
OY 566 AAGCATGCAATTTGACCGTGTACGCTCATATACATGTCACAGACATGAAAAA 625
DB 481 AAGCATGCAATTTGATCGTGTACGCTCATATACATGTCACAGACATGAAAAA 540
OY 626 TGGTGGACAGCTTGAAGAAAGCAATTTATCTTAATACGAGTAAAAAGTCAAAATCC 685
DB 541 TGGTGGACAGCTTGAAGAAAGCAATTTATCTTAATACGAGTAAAAAGTCAAAATCC 600
OY 686 AAGACATTTGCCACTACTGAGAAAGTCTTAAACCAACACGCTCATTAATCTATTTG 745
DB 601 AAGACATTTGCCACTACTGAGAAAGTCTTAAACCAACACGCTCATTAATCTATTTG 660
OY 746 CAGATGATGATGATGGAAGCACTTCAACCCCTGTTGAAACAGATGCTGTACTT 805
DB 661 CCAATGACGTTGATGGAAGCACTTCAACCCCTGTTGAAACAGATGCTGTACTT 720
OY 806 TCAATGTGTTGCTGCAAGGCGCAGGATTTGATCGTCTAAGCTATGCTTAAAG 865

```

```

DB 721 TCAATGTGTTGCTGTCACAAAGCTCCAGATTTGATGCCCTAAAGCTATGCTTGAAG 780
OY 866 AATTTGCTATCTTGACAGGTGTGTACAGTGTATACAGAGATCTAGACTTGAATTAAG 925
DB 781 AATTTGCTATCTTGACAGGTGTGTACAGTGTATACAGAGATCTAGACTTGAATTAAG 840
OY 926 ATGCTCAATGAAAGCCCTTGACAGGTGTGTACAGTGTATACAGTGTATTAAGATAGCAG 985
DB 841 ACGCTACAGATCCGACGCTGTGTGTACAGTGTATTAAGTACTGTATTAAGATAGCAG 900
OY 986 TAAATGGAAGGTGTAGAAAGTGTACAGATCTATGCTTAACCGCTATGCTGATTAAGT 1045
DB 901 TAAATGGAAGGTGTAGAAAGTGTCTAGAGCCATTCGCAACCGCTGTGCTGATTAAGT 960
OY 1046 CCAATTTAGAAACAAACACTCTGACTTTGACCTGGAAGAAACATCAAGAGCTTGGCA 1105
DB 961 CACAACCTAGAAACCAACAGCTCTGACTTTGACCTGGAAGAAATTCAGAGAGCTTGGCA 1020
OY 1106 AATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1165
DB 1021 AATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
OY 1166 AATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1225
DB 1081 AATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
OY 1226 TCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1285
DB 1141 TCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
OY 1286 TGAAGGCGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1345
DB 1201 TGAAGGCGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
OY 1346 GTCAAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1405
DB 1261 GTCAAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
OY 1406 GCGCTGCAAGACAGATTTAAATGCTGCAACAGGTGAGTGGTGAATGATTAAGAAACG 1465
DB 1321 GCGCTGTTGAAGACGCTTTAAATGCTGCAACAGGTGAGTGGTGAATGATTAAGAAACG 1380
OY 1466 GAATCATTTGACCTGTCNAAGTAAACAGATCAGC 1499
DB 1381 GAATCATTTGACCTGTCNAAGTAAACAGATCAGC 1414

```

```

RESULT 12
AF389514      2054 bp   DNA      linear      BCT 02-JUL-2002
LOCUS        AF389514
DEFINITION   Streptococcus bovis GroES gene, complete cds; and GroEL gene,
ACCESSION   AF389514
VERSION      AF389514.1
KEYWORDS     GI:21666288
SOURCE       Streptococcus bovis.
ORGANISM     Streptococcus bovis.
REFERENCE    1 (bases 1 to 2054)
AUTHORS      Teng, L.-J.
TITLE        The groESL genes of Streptococcus bovis
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 2054)
AUTHORS      Teng, L.-J.
TITLE        Direct submission
JOURNAL      Submitted (08-JUN-2001) School of Medical Technology, National
Taipei University College of Medicine, No. 1, Chang-te Street,
Taipei 100, Taiwan
FEATURES     Location/Qualifiers
source       1..2054
              /organism="Streptococcus bovis"
              /db_xref="taxon:1315"

```

CDS	92..376	/codon_start=1	
		/transl_table=1	
		/product="GroES"	
		/protein_id="AA073641.1"	
		/db_xref="gi:2166289"	
		/translation="MKRPIDPVLKKEPEQDTGCGFVLAGASKEKENTQATVAVGD GARTLGEVAPSVAAQDKVILENVGILEVADNDNTVITVEADITLTA"	
	444..2054		
CDS		/codon_start=1	
		/transl_table=1	
		/product="GroEL"	
		/protein_id="AA073642.1"	
		/db_xref="gi:2166290"	
		/translation="MAKDIFSDARASMKRGVDIADTVKVLGPKGRNVYLEKSEF SPITNDVTLAKEIELEDFENMGAKLVSEVASKNIDADDTTATVTOAIVREG LKNVTGANPTGIRGIESVAVADLKAIAQPAVANKEAIAQVAAVSSSEKVEYI SEAKRVGNDVYITIEESRQMETLDVVEGMDRQVLSQYVTDNKKVADLENPYI LIDDKRISIDILPLEEVLTSRPLIADVDGEALPTLVANKIRGFNVAVFA PGFGRKRAMLEDIAVLGTGTVITEDLDLKDANNTALGOAAKVDSDSVIVEGA GEASSIANKRVNIVISOLEATTSEDFREKLEKLAGVAVIKVGAATETLKMKL RIEDALNATRAVVEGIVAGGTALVINYISKVAIELEGDDEATGRNIVLRLEEFVQ IAFNAGYEGSVIIEHLKNSGVGTGNANSEVNMVVEAGIIDPVKTRSAIONASVA SLITTEVAVNHEPAPAPAPAPMPDS"	
BASE COUNT	652 a 361 c 472 g 569 t		
ORIGIN			
Query Match	67.4% Score 1104.2; DB 1; Length 2054;		
Best Local Similarity	80.7% Pred. No. 1.5e-215;		
Matches 1289; Conservative	0; Mismatches 308; Indels 0; Gaps 0;		
OY	1	ATGGCAAAAGAAATCAATTTTCAGACAGATGCCGCTGCTGATAGTGGCGAGATTGAT	60
DB	444	ATGGCAAAAGATTAATTTTCAGACAGATGCCGCTGATAGTGGCGAGATTGAT	503
OY	61	ATGTAGCAGATACCGTCAAGTAACGCTGCTCTAAAGGCGCAATTTGTTCTTGA	120
DB	504	ATTTGGCAGATACCGTCAAGTAACGCTTAGGCCCTAAAGCTCTAACTGTTCTTGA	563
OY	121	AAAGCTTTGCTCCCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	180
DB	564	AAATCAATTTGCTCCCTTAATTAATTAATTAATTAATTAATTAATTAATTAAT	623
OY	181	TTAGAGATCAATTTTGAATCAATGAGGAGCAAAATGCTGCTGATCAATCAATCA	240
DB	624	TTAGAGACCAATTTTGAATCAATGAGGAGCAAACTGCTGATCAATCAATCAAT	683
OY	241	AATGATATTGCTGCTGATGAGGAGCAATCAATGAGGAGCAATCAATCAATCAAT	300
DB	684	AACGACATCGCTGCTGATGAGGAGCAATCAATGAGGAGCAATCAATCAATCAAT	743
OY	301	GAAGGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	360
DB	744	GAAGGCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	803
OY	361	ACAGCAGACAGACAGCTGTGAAGCCTTGAAGCCTTGAAGCCTTGAAGCCTTGA	420
DB	804	TCAGCTGCTGCTGCTGATGAGGAGCAATTAATTAATTAATTAATTAATTAATTA	863
OY	421	GAAGTATTGCTGCTGCTGATGAGGAGCAATTAATTAATTAATTAATTAATTAAT	480
DB	864	GAAGGATGCTGCTGCTGATGAGGAGCAATTAATTAATTAATTAATTAATTAAT	923
OY	481	TCAGAGCTATGAGGCTGTGAGGAGCAATTAATTAATTAATTAATTAATTAATTA	540
DB	924	TCAGAGCTATGAGGAGCTGTGAGGAGCAATTAATTAATTAATTAATTAATTAAT	983
OY	541	ATGGAAGCAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	600
DB	984	ATGGAAGCAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1043
OY	601	TACATGCTCAGACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	660
DB	1044	TACATGCTCAGACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1103
OY	661	ACGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	720
DB	1104	ACGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1163
OY	721	ACCAACCTGCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	780
DB	1164	ACTATGCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1223
OY	781	GCTTGAACCAAGATTCGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTA	840
DB	1224	GCTTGAACCAAGATTCGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTA	1283
OY	841	GATGCTGCTAAAGCTATGCTGAAGCAATTCCTTATTCGACAGGCTGATGATTA	900
DB	1284	GACGCTGCTAAAGCAATTCCTTATTCGATTCGCTTAACTGCTGATGATTAATTA	1343
OY	901	GAGGCTGCTAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	960
DB	1344	GAAAGCTGCTGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1403
OY	961	ATTGACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1020
DB	1404	GTAAGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1463
OY	1021	GCTAACCTTATTCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1080
DB	1464	GCTAACCTTATTCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1523
OY	1081	GAATACTAAGAAAGCTTTGGGAAATTAATTAATTAATTAATTAATTAATTAATTAAT	1140
DB	1524	GAATACTAAGAAAGCTTTGGGAAATTAATTAATTAATTAATTAATTAATTAATTAAT	1583
OY	1141	GCTCAACAGAGACGCTTTAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAAT	1200
DB	1584	GCACGCGACAGAAACGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1643
OY	1201	ACAGCTGACGCTGTAAGAAAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1260
DB	1644	ACAGCTGACGCTGTAAGAAAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1703
OY	1261	ATTGAAAGGAGAGAGCTTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1320
DB	1704	ATTGAAAGGAGAGAGCTTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1763
OY	1321	CTTGCTGCTGTAAGAGGCTGATGCTCAATTTGCTTAAATGCTGCTGCTGCTGCTGCTG	1380
DB	1764	CTTGCTGCTGTAAGAGGCTGATGCTCAATTTGCTTAAATGCTGCTGCTGCTGCTGCTG	1823
OY	1381	GTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1440
DB	1824	GTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1883
OY	1441	GAGTGGCTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1500
DB	1884	GAGTGGCTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1943
OY	1501	CTTCAAAATGAGGCTGCTGATGCTTAAATTAATTAATTAATTAATTAATTAATTAAT	1560
DB	1944	CTTCAAAATGAGGCTGCTGATGCTTAAATTAATTAATTAATTAATTAATTAATTAAT	2003
OY	1561	AAACCTGAACCACTACCGCAGCGCCAGCAATCGCAG	1597
DB	2004	CATCGAAGCAAGCTGACCGACGCGCAGCTCGAG	2040
RESULT 13			
AY121363			
LOCUS	AY121363	1384 bp	DNA linear BCT 30-JUL-2002
DEFINITION	Streptococcus dysgalactiae subsp. dysgalactiae strain ATCC 43078		
Chaperonin GroEL gene, partial cds.			
ACCESSION	AY121363		

```

VERSION          AV121363.1  GI:22022485
KEYWORDS
SOURCE
ORGANISM          Streptococcus dysgalactiae subsp. dysgalactiae.
                  Streptococcus dysgalactiae subsp. dysgalactiae
                  Bacteria: Firmicutes; Lactobacillales; Streptococcaceae;
                  Streptococcus.
REFERENCE         1 (bases 1 to 1384)
AUTHORS           Moo, P.C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W.,
                  Tse, H., Hong, K.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.
TITLE             Chapterin GroEL gene of Group C Streptococcus dysgalactiae
                  subsp. dysgalactiae
JOURNAL           Unpublished
AUTHORS           Moo, P.C.Y., Teng, J.L.L., Lau, S.K.P., Lum, P.N.L., Leung, K.-W.,
                  Tse, H., Hong, K.-L., Li, K.-W., Lam, K.-C. and Yuen, K.-Y.
TITLE             Direct Submission
JOURNAL           Submitted (12-JUN-2002) Microbiology, The university of Hong Kong,
                  Pokfulam Road, Hong Kong, China
FEATURES
source            1..1384
                  /organism="Streptococcus dysgalactiae subsp. dysgalactiae"
                  /strain="ATCC 43078"
                  /sub_species="dysgalactiae"
                  /db_xref="ATCC:43078"
                  /db_xref="taxon:99822"
                  <1..>1384
                  /codon_start=3
                  /transl_table=11
                  /product="Chaperonin GroEL"
                  /protein_id="AA083126.1"
                  /db_xref="GI:22022486"
                  /translation="NVYLEKAFSGPLITNDGVITAKELIEDHFEENKARLVSEVASK
                  TNDIAGDTTATVLTGAIIVREGILANTVAGANPDIIGRIETAAITVALALAIOPY
                  SGREAIQVAOVAVSSRSSEKVEYISEMERVNGNGVITTEBERGFELEVEGKQFDR
                  GYSOYVTVNKEKVADELPILITDOKKSNIDITLPLEBEVKTREPLLIADVDY
                  GEAIPLVLNKIRGTENVVAAPGFGRKRALEIDILGGLVIEDLELIDAT
                  MPALGOAAVTVDSQVIVEGAGSSEAIANRGLIKSQLSTTTSDEDEKIQEELK
                  LAGGAVIVGATETALKEMLRIEDALNATVAEGLIYAGGGTILITALEKVAL
                  ELGDGATGRNIVIRALEBEVRQIFNAGEGSVVIDKLKSPVGTGFNAATGEWVDV
                  IAAGIIDPKYK"
BASE COUNT        397 a      269 c      349 g      369 t
ORIGIN
Query Match       65.9%; Score 1080; DB 1; Length 1384;
Best Local Similarity 86.3%; Pred. No. 1,4e-210;
Matches 1194; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

```

```

Db 361 AGCTTGAGAAATACATTTTCAGAACCCATGGAAACGTGGCTAATGACGGTCTCACTACTA 420
Oy 524 TCGAAGATCTCCAGGATATGGAACAGAACCTTGAAGTGGTGAAGCATGATTTGACC 583
Db 421 TCGAAGATCAGCTGATGAGACACACACTTGAAGTGGTGAAGCATGATTTGACC 480
Oy 584 GTGGTACCTGTCTCAATATACATGCTGCACAGACATGAAGAAATGCTTCAGACCTTGAAA 643
Db 481 GTGGTACCTGTCTCAATATACATGCTGCACAGACATGAAGAAATGCTTCAGACCTTGAAA 540
Oy 644 ACCCATTTATCTTAATACAGGATTAAGAAAGTGTCAACATCCAAAGACATTTTGCCACTAG 703
Db 541 ACCCATTTATCTTATCTTAATACAGGATTAAGAAAGTGTCAACATCCAAAGACATTTTGCCACTAG 600
Oy 704 TTGAGAGAGTCTTAACCAACAGCGTCCATCTTACATTTATGAGATGATGAGAGTGG 763
Db 601 TTGAGAGAGTCTTAACCAACAGCGTCCATCTTATGATTTATGCGCATGATGAGAGTGG 660
Oy 764 AAGCATTCCCAACCCCTGTCTTGACACAGATTCGTGACTTTCATATGCTGCTGTCA 823
Db 661 AAGCATTCCCAACCCCTGTCTTGACACAGATTCGTGACTTTCATATGCTGCTGTCA 720
Oy 824 AAGCAGCCAGATTTGGTATGCTGTGAAGAGTATGCTTGAAGACATTTCTTACAG 883
Db 721 AAGCAGCCAGATTTGGTATGCTGTGAAGAGTATGCTTGAAGACATTTCTTACAG 780
Oy 884 GTGGTACAGTATACAGAGATCTAGCACTTGAATTAAGATGCTACATGACAGCCC 943
Db 781 GTGGTACAGTATACAGAGATCTAGCACTTGAATTAAGATGCTACATGACAGCCC 840
Oy 944 TTGACAGAGCTGTCAAGATTCAGATTGATAAAGATACACAGATTTGTAAGTTGAC 1003
Db 841 TTGACAGAGCTGTCAAGATTCAGATTGATAAAGATACACAGATTTGTAAGTTGAC 900
Oy 1004 GAAGTACAGAGTATGCTTACGATGATGACATGATTAATGCAATTTGAAGAACAA 1063
Db 901 GAAGTACAGAGTATGCTTACGATGATGACATGATTAATGCAATTTGAAGAACAA 960
Oy 1064 CTCTGACTTGAAGCGTGAAGAACTCAAGAAAGCTTTGGGAAATTTACTGCTGCTG 1123
Db 961 CTCTGACTTGAAGCGTGAAGAACTCAAGAAAGCTTTGGGAAATTTACTGCTGCTG 1020
Oy 1124 CTGTTATCAAGTATGAGAGCTGCACAGACAGACGCTTTAAAGAAATGAACCTTGCA 1183
Db 1021 CTGTTATCAAGTATGAGAGCTGCACAGACAGACGCTTTAAAGAAATGAACCTTGCA 1080
Oy 1184 AGATGCTCTTAATGCTTACAGCTGCACAGCGCTTGAAGAGTATCGTCTGCTGCTGCA 1243
Db 1081 AAGAGCTTATGATCCACAGCGCTTGAAGAGTATCGTCTGCTGCTGCTGCTGCA 1140
Oy 1244 CAGACCTTATTAAGGCTTATGAAGAAAGTACAGCTTGAAGAGTATCGTCTGCTGCTGCA 1303
Db 1141 CAGACCTTATTAAGGCTTATGAAGAAAGTACAGCTTGAAGAGTATCGTCTGCTGCTGCA 1200
Oy 1304 CTGAGAGTAACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1363
Db 1201 CTGAGAGTAACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
Oy 1364 CTGAGAGTAACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1423
Db 1261 CTGAGAGTAACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
Oy 1424 TTAATGCTCAACAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1483
Db 1321 TTAATGCTCAACAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
Oy 1484 AAGT 1487
Db 1381 AAGT 1384

```

RESULT 14
AF389516

LOCUS AF389516 2324 bp DNA linear BCT 02-JUL-2002
DEFINITION Streptococcus mutans GroES gene, complete cds; and groEL gene,
partial cds.
ACCESSION AF389516
VERSION AF389516.1 GI:21666294
KEYWORDS
SOURCE Streptococcus mutans.
ORGANISM Streptococcus mutans
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
REFERENCE
Teng, L.-J.
1 (bases 1 to 2324)
The groEL genes of Streptococcus mutans
JOURNAL Unpublished
2 (bases 1 to 2324)
Teng, L.-J.
Teng, L.-J.
2 (bases 1 to 2324)
Direct Submission
Submitted (08-JUN-2001) School of Medical Technology, National
Taiwan University College of Medicine, No. 1, Chang-te Street,
Taipei 100, Taiwan
FEATURES
source
Location/Qualifiers
1..2324
/organism="Streptococcus mutans"
/db_xref="taxon:1309"
318..605
/codon_start=1
/transl_table=11
/product="GroES"
/protein_id="AA073645.1"
/db_xref="GI:21666295"
/translation="MKPLGDRVYVVKKEKQYGVLAGSDEKTKKQVYVANG
GVRLTGLVASSLAGQDTLLIENHGVTFKNDGDYILLIREDVLAIVND"
717..>2324
/codon_start=1
/transl_table=11
/product="groEL"
/protein_id="AA073646.1"
/db_xref="GI:21666296"
/translation="MKDIFKSDASSVRGVDLADYKVTLPGRNVYLEKSG
SPILINDGVTIAKELELEDHFNNGAKLVSEVASTNDIAGDGTATVLTQALVEG
LKNVTPAGNITGRILETAIVAVDELKAIAPVSKELIAQVAVSREKGEYV
SEANEKGVNDGVTTIEESRGMETLEVDYVQFSLQVYVNTNEMKVADELNYL
LITDKISNTQDVLPLEEVLKTRNPLLIADYDGLPFLVINKIGRTNVAVAKA
PGFGRKAMLEDIIVLTGTVTIEDLGLKDTTIALGOAAVYVNDSTVIVGS
GKEKAVNRVNLKSIETATSPDEKLEKQLKLSGVAVIKVGAETTELKMKL
RIEDALNATRAVEGIVAGGTALINVLEKVALDLTDPAATGNLVLRLPEPVR
LKNAGEGSVIIDKLNSSAGTFENANGENVIMIDAGILDPVVTSLQNAASVA
SLILTEPAVVDHPAPEAPAAPMPDS"
BASE COUNT 695 a 368 c 544 g 717 t
ORIGIN
Query Match 65.7% Score 1075.4; DB: 1; Length 2324;
Best Local Similarity 79.8%; Pred. No. 1.1e-209;
Matches 1268; Conservative 0; Mismatches 321; Indels 0; Gaps 0;
QY 1 ATGGCAAGAAATCAATTTTTCAGAGATGCGCGTCGTCGCCATGTCGCGGAGATTGAT 60
DB 717 ATGGCAAGAAATCAATTTTTCAGAGATGCGCGTCGTCGCCATGTCGCGGAGATTGAT 776
QY 61 ATGTAGACAGATACCGTCAAGTACGCTTGTCTTAAGGCGCAATGTTGTTCTTGA 120
DB 777 ATTTTACAGATACAGTAAAGTAACTTGGGCGCCCTTAAGAGCAAGATGTTCTTGA 836
QY 121 AAAGCTTTGTTCTCCCTTAATTAATGACGGGGTAAACCATGTTGAAGATCGAA 180
DB 837 AAGTCGTTGTTCTCCCTTAATTAATGACGGGGTAAACCATGTTGAAGATCGAA 896
QY 181 TTAAGATCATTTTGAAGACATGAGCAAAATTTGTCGAGAGTGGCTTAAACC 240
DB 897 TTAAGATCATTTTGAAGACATGAGCAAAATTTGTCGAGAGTGGCTTAAACC 240
QY 241 AATGATTTGCTGTGATGGAGACTACTGACACGTTTACACAGCATTTGTCAT 300
DB 2037 CTTGCTGCTGTGATGGAGACTACTGACACGTTTACACAGCATTTGTCAT 300

DB 957 AATGATTTGCTGTGATGGAGACTACTGACACGTTTACACAGCATTTGTCAT 1016
QY 301 GAAGACATAAAATGTGACAGACAGTCTTATTCATATGTTATCGTCGAGCATTTGA 360
DB 1017 GAAGACATAAAATGTGACAGACAGTCTTATTCATATGTTATCGTCGAGCATTTGA 1076
QY 361 ACAGCAACAGCAAGCTGTGTAAGCTTGAAGCCATGCTCAACCTGATGTGCAAG 420
DB 1077 ACAGCAACAGCAAGCTGTGTAAGCTTGAAGCCATGCTCAACCTGATGTGCAAG 420
QY 421 GAAGCTATTGCTCAAGCTGCTGCAATATCATACGCTTGAAGAAAGTTGAGATATC 480
DB 1137 GAAGCTATTGCTCAAGCTGCTGCAATATCATACGCTTGAAGAAAGTTGAGATATC 480
QY 481 TCAGAGCTATGAGCGTGTGGCAACGATGTGATTAACATCGAAGATCTGAGGT 540
DB 1197 TCAGAGCTATGAGCGTGTGGCAACGATGTGATTAACATCGAAGATCTGAGGT 1256
QY 541 ATGGAACAGAACTGTAAGTGTGTAAGGCTGATTTGACGCGTGTACCTGTCTCA 600
DB 1257 ATGGAACAGAACTGTAAGTGTGTAAGGCTGATTTGACGCGTGTACCTGTCTCA 600
QY 601 TACATGTCACAGACATTAAGAAATGTTGACAGCTTGAAGAAAGTTGAGATATC 660
DB 1317 TACATGTCACAGACATTAAGAAATGTTGACAGCTTGAAGAAAGTTGAGATATC 660
QY 661 ACAGATAAAAGTGTCAAAACATCCAGACATTTGCCACTGATGAGAGTCTTAA 720
DB 1377 ACAGATAAAAGTGTGTAAATTTCAAGATGTTCTTCCGCTTGAAGAAAGTTCTTAA 720
QY 721 ACAGACCTGCTATTAATTAATTCAGATGATGTGATGATGATGATGATGATGAT 780
DB 1437 ACAGACCTGCTATTAATTAATTCAGATGATGTGATGATGATGATGATGATGAT 780
QY 781 GCTTGAACAGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 1497 GCTTGAACAGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 841 GATCGTGTGAAGTATGCTGAAGACATGCTGATCTGATGATGATGATGATGATGAT 900
DB 1557 GATCGTGTGAAGTATGCTGAAGACATGCTGATCTGATGATGATGATGATGATGAT 900
QY 901 GAGGATGAGACCTGATTAATTAAGATGATGATGATGATGATGATGATGATGATGAT 960
DB 1617 GAGGATGAGACCTGATTAATTAAGATGATGATGATGATGATGATGATGATGATGAT 960
QY 961 ATTACAGTTTAAAGTATGACACAGTATGATGATGATGATGATGATGATGATGAT 1020
DB 1677 ATTACAGTTTAAAGTATGACACAGTATGATGATGATGATGATGATGATGATGAT 1020
QY 1021 GCTAACCTATGCTGATTAATTCGCAATTAAGAAACACATGCTGATGATGATGAT 1080
DB 1737 GCTAACCTATGCTGATTAATTCGCAATTAAGAAACACATGCTGATGATGATGAT 1080
QY 1081 GAAATACATCAAGAGTGTGCGAAATTAAGTATGATGATGATGATGATGATGATGAT 1140
DB 1797 GAAATACATCAAGAGTGTGCGAAATTAAGTATGATGATGATGATGATGATGAT 1140
QY 1141 GCTCCACAGACAGCTTAAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAA 1200
DB 1857 GCAAGACAGAAACAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAA 1200
QY 1201 ACAGCTGAGCGCTGTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAAT 1260
DB 1917 ACAGCTGAGCGCTGTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAAT 1260
QY 1261 ATTGAAAAATGACAGCTTGTGAGCTGAGAGGATGATGATGATGATGATGATGAT 1320
DB 1977 ATTGAAAAATGACAGCTTGTGAGCTGAGAGGATGATGATGATGATGATGATGAT 1320
QY 1321 CTTGCTGCTGTGATGAGAGCTGTACGTAATGCTTAAATGCTGAGTGAAGAGCTTC 1380
DB 2037 CTTGCTGCTGTGATGAGAGCTGTGTCCGTAATGCTTAAATGCTGAGTGAAGAGCTTC 2096

QY 1381 GTAGTTATGACAGTGGAAAAACGCCCTGCGAGACAGATTAACTGCAACAGGT 1440
DB 2097 GTGATTATGATTAATTAATGACAGAGTACAGAGTTCAATGCTGCAACGGG 2156
QY 1441 GAGTGGGTATGATTAATTAATGACAGAGTACAGAGTTCAATGCTGCAACGGG 1500
DB 2157 GAGTGGGTATGATTAATGACAGAGTACAGAGTTCAATGCTGCAACGGG 2216
QY 1501 CTTCAAAATGACAGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1560
DB 2217 CTTCAAAATGACAGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 2276
QY 1561 AATCGTGAACAGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1589
DB 2277 CATCGACTGACAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2305

RESULT 15
AF389515 2320 bp DNA linear BCT 02-JUL-2002
LOCUS Streptococcus intermedius GroES gene, complete cds; and GroEL gene,
DEFINITION partial cds.
ACCESSION AF389515 GI:21666291
VERSION AF389515.1 GI:21666291
KEYWORDS
SOURCE
ORGANISM Streptococcus intermedius.
Streptococcus intermedius.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
REFERENCE 1 (bases 1 to 2320)
Teng/L.-J.
The groES genes of Streptococcus intermedius
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 2320)
Teng/L.-J.
DIRECT SUBMISSION
Submitted (08-JUN-2001) School of Medical Technology, National
Taiwan University College of Medicine, No. 1, Chang-te Street,
Taipei 100, Taiwan
FEATURES
Location/Qualifiers
source 1..2320
/organism="Streptococcus intermedius"
/db_xref="taxon:1338"
405..686
/codon_start=1
/transl_table=1
/product="GroES"
/protein_id="AAW73643.1"
/db_xref="GI:21666292"
/translation="MKRPLGDRVLEFVEKREKVGFGVYAGAGDRTAKRYAVAGSG
IRLNGELVAPSVAKGDTYVLESHGTEVVDSEKLVVNEVNLALIVE"
719..>2320
/codon_start=1
/transl_table=1
/product="GroEL"
/protein_id="AAW73644.1"
/db_xref="GI:21666293"
/translation="MAADIKFSADARSAMVGVLIADTVAVTLGPKRHNVLKESFG
SPILINDVITAKETIELEDFENMGAKLVSEVASTNDIADGTTAAVLTQALVRG
IKNVAIVGNDGVIIRIESEKMDTELDVSEMGQDSEGYSTQVTDNEKVVADLNPYI
SEAMEVGNDSVITIESEKMDTELDVSEMGQDSEGYSTQVTDNEKVVADLNPYI
LITDKKISNIOELPLENLIKTSRPLLIADVDGEALPTVLNKIRGTFPVYAVAG
PGGRKRAMLEDAIILITGVITEDLEKAPATKALGQASKVTVDSDIVYVAG
GDAEAIARVAIVKISQIESVTSERPEKLOERAKLSGSAVTKVGAATETLEKML
RIDALNTRAAVEGIVSGGTAFVAVDAVALELSDADATGRNRYIRALHEPVYD
IALNAGFSGIVIDRLKNSGVGTGNAATGEMNINIEGIIIDPVKTRHSLQNASVA
SLITTEAVVASOPEPASPAPAMPSP"

BASE COUNT 731 a 408 c 527 g 654 t

Query Match 65 2% Score 1068.2; DB 1: Length 2320;
Best Local Similarity 79.2% Pred. No. 3.2e-208;

Matches 1268; Conservative 0; Mismatches 333; Indels 0; Gaps 0;
QY 1 ATGGCAAAAGAAATCAAAATTTTCACAGATCCGCTGCTCCAGTGGCCGAGATTAT 60
DB 719 ATGGCAAAAGAAATCAAAATTTTCACAGATCCGCTGCTCCAGTGGCCGAGATTAT 778
QY 61 ATGTAGCAGATACCGTCAAAAGTAAAGTGGTGTCTTAAAGGCGCATGTGTTGAA 120
DB 779 ATTTTTCAGATACCGTCAAAAGTAAAGTGGTGTCTTAAAGGCGCATGTGTTGAA 838
QY 121 AAAGCTTTTGGTCTCCCTTAATTAATTAAGAGGGGTAAACCATGCTTAAGATGAA 180
DB 839 AAATCATTTTGGTCTCCCTTAATTAATTAAGAGGGGTAAACCATGCTTAAGATGAA 898
QY 181 TTGAAGATCAATTTTGAAGAGGAGGAGCAAAATTTGGTCTTAAAGGCGCATGTG 240
DB 899 CTCGAAGATCAATTTTGAAGAGGAGGAGCAAAATTTGGTCTTAAAGGCGCATGTG 958
QY 241 AATGATTTCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
DB 959 AATGATTTCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1018
QY 301 GAAGCATTAATAAATGTGACAGAGTGTCTAATCCAAATTTGATCCGTCAGAGCAT 360
DB 1019 GAAGCATTAATAAATGTGACAGAGTGTCTAATCCAAATTTGATCCGTCAGAGCAT 1078
QY 361 ACAGCAACAGCAACAGCTGTGAAAGCCTTGAAGCCATTGCTCAACCTGATCGCAAG 420
DB 1079 ACAGCTGTGCAACAGCTGTGAAAGCCTTGAAGCCATTGCTCAACCTGATCGCAAG 1138
QY 421 GAAGCTATTTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 1139 GAAGCTATTTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1198
QY 481 TCAGAGCATTAAGAGGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
DB 1199 TCAGAGCATTAAGAGGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1258
QY 541 ATGCAACAGCAACATTAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
DB 1259 ATGCAACAGCAACATTAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1318
QY 601 TACATGTGTCACAGCAATGAAATTAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGG 660
DB 1319 TACATGTGTCACAGCAATGAAATTAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGG 1378
QY 661 ACAGTAAATAAAGTGTCAACATCAAGAGATTTTGGCACTTGTGAGAGTGTCTTAA 720
DB 1379 ACAGTAAATAAAGTGTCAACATCAAGAGATTTTGGCACTTGTGAGAGTGTCTTAA 1438
QY 721 ACCAAGCGTCATTAATCATTAATGAGATGATGATGATGATGATGATGATGATGAT 780
DB 1439 ACCAAGCGTCATTAATCATTAATGAGATGATGATGATGATGATGATGATGATGAT 1498
QY 781 GTCTTGAACAGATTCGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 840
DB 1499 GTCTTGAACAGATTCGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1558
QY 841 GATGCTGTGAAGCTTAATGCTTGAAGCAATGCTTGTGAGAGGAGTGAAGTATTA 900
DB 1558 GATGCTGTGAAGCTTAATGCTTGAAGCAATGCTTGTGAGAGGAGTGAAGTATTA 1618
QY 901 GAGCATGAGAGCTTGAATTAAGATGCTAATGACAGCCCTTGAAGAGGCTGCTAAG 960
DB 1619 GAGCATGAGAGCTTGAATTAAGATGCTAATGACAGCCCTTGAAGAGGCTGCTAAG 1678
QY 961 ATTACAGTGTGAATGATGACAGAGTATGTTGAAGGTTGAGAGGAGTGAAGAGTAT 1020
DB 1679 ATTACAGTGTGAATGATGACAGAGTATGTTGAAGGTTGAGAGGAGTGAAGAGTAT 1178
QY 1021 GCTAACCGGATTTGCTGATTAATGCAATTAAGAAACAACTTGTGATGACCGT 1080
DB 1739 GCTAACCGGATTTGCTGATTAATGCAATTAAGAAACAACTTGTGATGACCGT 1798

